SUPPORTING INFORMATION

Weighted protein interaction network analysis of Frontotemporal Dementia.

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Table S1. Original "Interaction Detection Methods" and methods re-assignment for the analysis. The detection interaction methods that we removed because 'generic' are highlighted in gray.

Table S2. g:Profiler enrichment and semantic classes organization for the enrichment of the entire FTD-PN against the "all genome reference dataset" and the "brain-only reference dataset". Semantic classes reported in pink are present in the "all genome" analysis but not in the "brain-only" analysis. Semantic classes reported in blue are present in the "brain-only" but not in the "all genome" analysis.

Table S3. g:Profiler enrichment and semantic classes organization for the enrichment of the entire FTD-PN against the "all genome reference dataset" and the "brain-only reference dataset". Semantic classes reported in pink are present in the "all genome" analysis but not in the "brain-only" analysis. Semantic classes reported in blue are present in the "brain-only" but not in the "all genome" analysis.

Table S4. Comparison of the enrichment results between gProfiler, Panther and Webgestalt. The per-mil of enrichment is calculated referring to the total amount of enriched terms and is color-coded in red. Missing semantic classes are highlighted in pink.

Table S5. Comparison between the enrichment of the FTD-PN-IIH connecting over 8 interactomes (29 nodes) and the Albinism network (79 nodes). The per-mil of enrichment is calculated referring to the total amount of enriched terms and is color-coded in red. Overlapping semantic classes are highlighted in pink. Semantic classes exclusive to albinism are highlighted in blue and the specific GO-BP terms are listed at the bottom of the table.

Table S6. Table containing the relevant semantic classes as indicated by the enrichment of the IIHs.

Table S7. List of protein-IDs indicating proteins from the FTD-PN that contribute to enrichment of DNA damage control, gene expression regulation and waste disposal both in W-PPI-NA and WGCNA. IIHs are color-coded in red.

Figure S1. Examples of entries removed from the imput data (old protein identifiers, non-human taxid, non-defined detection interaction method and/or Pubmed identifier).

Figure S2 to S27. IIHs with their surrounding interactors and degree of connectivity across the interacomes of multiple seeds. Any IIH could either be: i) a seed; ii) a 1st layer interactor or; iii) a 2nd layer interactor. Provided that only VCP was an IIH and a seed, any IIH was actually either a 1st or 2nd layer interactor. When the IIH was part of the 1st layer of the FTD network, then its surroundings would include: seed(s) (highlighted in green) + 1st layer neighbors present in the first layer of the network and connected directly to the seeds (highlighted in blue) + 2nd layer neighbors (highlighted in purple and for which the IIH would be the "seed"). When the IIH was part of the 2nd layer of the FTD network, then its surroundings would only include seed(s) (highlighted in green) + 1st layer neighbors

connected directly to the seeds (highlighted in blue). As in the latter case the IIH would not be a "seed" for any interactome, the nodes highlighted in purple are absent.

Figure S28 to S40. The graph reports the percentage of GO-BP terms as distributed in subclasses inside each single semantic class.

Figure S41 to S44. Graphs showing the contribution of the interactome (1st + 2nd layers) of each seed towards the enrichment of specific semantic classes. The semantic classes are part of functional blocks indicating phase transition, development/proliferation of epthelium, DNA damage repair, protein localization. The gray bars indicate the weighted threshold for each single interactome. Points above that threshold are considered to highly contribute towards enrichment. Interactomes contributing to enrichment are indicated by the arrows.

Figure S45. Heatmap reporting the importance of each interactome towards enrichment of each specific semantic class. Red = high involvement; orange = mid-high involvement; yellow = mid-low involvement, and; white = low involvement.

File S1. ID conversion table

File S2. Enrichment – gProfiler – entire network

File S3. Enrichment – gProfiler – IIHs

COSP	Group Name	Members	Code
	Co-immunoprecipitation	Co-immunoprecipitation Anti-ball colif	MI:0019 MI:0006
		Anti-tag coli [®] Immunodepleted colimnunoprecipitation	MI:0007 MI:0858
APMS	Affinity Purification Mass Spectrometry	Pull Down	MI:0096
		Tandem Affinity Puritication GST Pulldown	MI:0676 MI:0059 MI:0004
		Affinity Chromatography Affinity Technology	MI:0400
		Chromatography technology His pull down	MI:0091 MI:0061
		Interactionse parallel affinity capture	MI:0963
t	Enzymatic Assay (Generic)	Enzymatic Assay Protein Kinase Assay	MI:0415 MI:0424
		Phosphatase Assay Fluorescence Phosphatase Assay	MI:0434 MI:1019
		Clevage Assay In-gel kinase assay	MI:0990 MI:0423
		Protease assay	MI:0435
		Cleavage reaction Dephosphorylation reaction In gel phosphatase assay	MI:0194 MI:0203
			MI:0514 MI:0953
		Phosphotransferase assay Kinase scintillation proximity assay	MI:0841 MI:0425
SE	Enzymatic Assay (Specific)	Sumoviation reaction	MI.0566
		Deacetylase assay Neddylase assay	MI:0106 MI:1010
		Acetylation reaction Acetylase assay	MI:0192 MI:0889
UE	Enzymatic Assay (Specific)	Ubiquitination Reaction	MI:0220
		Ubiquitin Binding Ubiquitinase Assay	MI:0443 MI:0997
		Deubiquitinase assay	MI:0998
PA	Arrays	Protein Array Peptide Array	MI:0089 MI:0081
		Array technology	MI:0008
		Antibody array	MI:0678 MI:0047
rw	Far-Western-Blot	Far-Western-Blot Anti tag western blot	MI:0047 MI:0705
co	Comigration	Comigration in gel electrophoresis	MI:0807
		Comigration in SDS-PAGE Comigration in nn denaturing gel elect.	MI:0808 MI:0404
		Blue Native page Electrophoresis Mobility Shift Assay	MI:0276 MI:0413
		Electrophoresis mobility based method Electrophoretic mobility supershift assay	MI:0982 MI:0412
DT	Display technology		M10034
		Display Technology Phage Display T7 Phage Display	MI:0084 MI:0108
		T7 Phage Display Lambda Phage Display Filamentous Phage Display	MI:0108 MI:0066 MI:0048
		Bacterial Display	MI:0009
		Yeast display	MI:0115
CX	Cross-linking	Cross-linking Protein CX with Bifunctional Reagent	MI:0030 MI:0031
MS	Molecular Sieving	Molecular Steving	MI:0071
FB	Filter Binding	Filter Binding	Mt:0049
C5	Cosedimentation	Cosedimentation Cosedimentation in solution	MI:0027 MI:0028
		Cosedimentation in solution Cosedimentation through density gradient	MI:0028 MI:0029
EUSA	ELISA	ELISA	MI:0411
CIP	Chromatin IP	Chromatin IP Assay	MI:0402
GTP	GTP/GDP Exchange assay	GTP/GDP Exchange assay	MI.0949
		GTPase assay	MI:0419
		g Luminescence Based Mam Interactionie Mapping	MI:0729
PX	Proximity Ligation Assay	Proximity Ligation Assay Proximity-dependent biotin identification	MI:0813 MI:1314
		Amplified luminescent proximity homogeneous assay	MI 0905
CD	Circular Dichrolum	Circular Dichroism	MI:0016
NMR	Nuclear Magnetic Resonance	Nuclear Magnetic Resonance Solid state nmr	MI:0077 MI:1104
×	X-ray cristallography	X-ray cristallography	MI:0314
	a ray commission of	X-ray scattering	MI:0826
SPR	Surface Plasmon Resonance	Surface Plasmon Resonance Surface plasmon resonance array	MI:0107 MI:0921
FT	Fluorescence Technology	Fluorescence Technology	MI:0051
		Bimolecular Fluo. Complementation Fluorescence Correlation Spectroscopy	MI:0809 MI:0052
		Classical Fluorescence Spectroscopy	MI:0017
		Fluorescence Resonance Energy Transfer Fluorescence Polarization Spectroscopy	MI:0053
		Biolyminescence resonance energy transfer Homogeneous time resolved fluorescence	MI:0012 MI:0510
	17/17/1	Fluorescense recovery after photobleaching	AR:1016
US	Light Scattering	Light Scattering Dynamic Light Scattering	MI:0067 MI:0038
CAL	Isothermal Tritation Calorimetry	Isothermal Tritation Calorimetry	MI:0065
MS	Mass Spectrometry	MS of complexes	
		Ms or compreses Detection by MS	MI:0069
			MI:0069 MI:0943
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Against ALL		5000	Against BRAIN ONLY		5000		
ADHESION		%	ADHESION		%		
adhesion	8	32.0	adhesion cell-cell	7	28.0		
cell-cell cell-substrate	5	20.0	cell-cell	3	12.0		
adherens-junction	4	16.0	adherens-junction	4	16.0		
cell-matrix	2	8.0	cell-matrix	2	8.0		
total	25	100	total	22	88		
CELL CYCLE		%	CELL CYCLE		%		
cell cycle	20	17.9	cell cycle	17	15.2		
segregation/cytokinesis	21	18.8	segregation/cytokinesis	15	13.4		
mitotic phase transition	13	11.6	mitotic phase transition	19	17.0	RNA METABOLISM	
cytoskeleton	13	11.6	cytoskeleton	11	9.8	RNA - metabolism	30
DNA - damage checkpoint	12	10.7	DNA - damage checkpoint	15	13.4	gene silencing	16
G1/S phase transition	9	8.0	G1/S phase transition	0	0.0	translation	13
enzymes	6	5.4	enzymes	4	3.6	RNA - spilicing	12
checkpoint	5	4.5	checkpoint	5	4.5	transcription - pol II promoter	12
G2/M phase transition	4	3.6	G2/M phase transition	0	0.0	transcription	11
DNA - damage checkpoint G1	4	3.6	DNA - damage checkpoint G1	0	0.0	RNA stability	9
ubiquitin-proteasome	4	3.6	ubiquitin-proteasome	0	0.0	gene expression	7
DNA - damage checkpoint G2	1	0.9	DNA - damage checkpoint G2	0	0.0	transcription factors	6
	100211	100.0		86	76.8	RNA - localization	6
total	112	100.0	total	86	76.8	transcription - pol I promoter	5
CELL DEATH		%	CELL DEATH		%	RNA - poly(A)	3
cell death	34	37.4	cell death	29	31.9	10000	77320
oxidative stress	15	16.5	oxidative stress	8	8.8	total	130
mitochondria	10	11.0	mitochondria	9	9.9		
extrinsic apoptosis	10	11.0	extrinsic apoptosis	10	11.0	SIGNALING	
enzymes	8	8.8	enzymes	7	7.7	signaling	46
intrinsic apoptosis	5	5.5	intrinsic apoptosis	5	5.5	cytokine	28
signaling	5	5.5	signaling	4	4.4	hormone	20
DNA damage	3	3.3	DNA damage	2	2.2	MAPK	17
ER stress	1	1.1	ER stress	1	1.1	interferon	16
						growth factor	12
total	91	100	total	75	82.4176	interleukin	12
		30000	Section 2012 Control of Control o		100000000000000000000000000000000000000	Wnt	11
CHROMATIN		%	CHROMATIN		%	toll-like	8
chromatin	10	21.7	chromatin	9	19.6	NFkappaB	7
telomers	13	28.3	telomers	11	23.9	TGF	5
histone - acetylation	8	17.4	histone - acetylation	6	13.0	Fc	5
histone	5	10.9	histone	4	8.7	ERBB	4
histone - methylation	4	8.7	histone - methylation	4	8.7	insulin	4
histone ubiquitin	4	8.7	histone ubiquitin	3	6.5	JNK	4
histone - phosphorylation	2	4.3	histone - phosphorylation	2	4.3	ERK	3
total	46	100.0	total	39	84.8	JUN	3
						TOR	2
DEVELOPMENT		%	DEVELOPMENT		%	chemokine	2
development	115	67.3	development	93	54.4	catenin	1
neuronal	15	8.8	neuronal	11	6.4	ephrin	1
brain	11	6.4	brain	8	4.7	hippo	1
neuronal - axon	8	4.7	neuronal - axon	6	2.3	integrin	1
glia	5	3.5	glia	4	0.0	neurotrophin	1
cell projection cell-proliferation	4	2.9	cell projection cell-proliferation	4	2.3	NOD	1
epith. cell-proliferation	5	2.9	epith. cell-proliferation	4	2.3	TRK	1
stem cell-proliferation	2	1.2	stem cell-proliferation	1	0.6		
total	171	100	total	131	76,6082	total	218
total	1/1	100	total	131	76.6082	STRESS	
DNA METABOLISM		%	DNA METABOLISM		%	stress	11
metabolism	24	35.3	metabolism	22	32.4	cell death	16
repair	18	26.5	repair	12	17.6	response to oxigen	8
DNA - damage checkpoint	12	17.6	DNA - damage checkpoint	15	22.1	response to radiation	8
damage	6	8.8	damage	4	5.9	oxidative stress	12
DNA - damage checkpoint G1	4	5.9	DNA - damage checkpoint G1		0.0	ER - stress	2
damage cell death	3	4.4	damage cell death	2	2.9		
DNA - damage checkpoint G2	1	1.5	DNA - damage checkpoint G2		0.0	total	57
total	68	100.0	total	55	80.9	TRANSPORT	
						transport nuclear transport	43 25
IMMUNE SYSTEM		%	IMMUNE SYSTEM		%	nuclear transport endocytosis	13
immune system	25	16.0	immune system	22	14.1	endocytosis exocytosis	12
cytokine	28	17.9	cytokine	23	14.7	vesicle - transport	12
lymphocytes	26	16.7	lymphocytes	23	14.7	transport of organelles	7
leukocytes	19	12.2	leukocytes	19	12.2	transport or organises	6
interferon	16	10.3	interferon	13	8.3	cytoskeleton - cell projection	5
interleukin	12	7.7	interleukin	9	5.8	ER - transport	3
antigen presentation	10	6.4	antigen presentation	10	6.4	cytoskeleton - based movement	3
innate	7	4.5	innate	7	4.5	Golgi -vesicle	1
receptors	7	4.5	receptors	7	4.5	transport of chromosomes	1
differentiation chemokine	4 2	2.6	differentiation chemokine	4	2.6	transport or chromosomes	,
		5007	100000000000000000000000000000000000000	1.0220		total	131
total	156	100	total	137	87.8205	WASTE DISPOSAL-QC	
LOCALIZATION		%	LOCALIZATION		%	ubiquitin-proteasome	34
localization	24	44.4	localization	28	51.9	autophagy	12
protein localization - nucleus	13	24.1	protein localization - nucleus	7	13.0	ubiquitin-proteasome - ER	7
rotein localization - membrane	10	18.5	protein localization - membrane	10	18.5	UPR	6
otein localization - mitochondria	4	7.4	protein localization - mitochondria	4	7.4	cell cycle	4
protein localization - ER	3	5.6	protein localization - ER	3	5.6	histone ubiquitination	4
	200	77.25000	100000	2.374	2500	ubiquitin-proteasome - SCF	1
total	54	100.0	total	52	96.3		
		- 1	I			total	68

RNA METABOLISM RNA - metabolism gene silencing translation RNA - splicing transcription - pol il promoter transcription - pol il promoter transcription RNA stability gene expression transcription factors	30 16 13 12	% 23.1 12.3	RNA METABOLISM RNA - metabolism	28	% 21.5
gene silencing translation RNA - spilicing transcription - pol ii promoter transcription RNA stability gene expression transcription factors	16 13 12	12.3			24 5
translation RNA - spilicing transcription - pol li promoter transcription RNA stability gene expression transcription factors	13 12				
RNA - spilicing transcription - pol II promoter transcription RNA stability gene expression transcription factors	12		gene silencing	10	7.7
transcription - pol II promoter transcription RNA stability gene expression transcription factors		10.0	translation	10	7.7
transcription RNA stability gene expression transcription factors		9.2	RNA - spilicing transcription - pol II promoter	8	6.2
RNA stability gene expression transcription factors	11	8.5	transcription - pol II promoter transcription	10	7.7
gene expression transcription factors	9	6.9	RNA stability	7	5.4
transcription factors	7	5.4	gene expression	8	6.2
	6	4.6	transcription factors	5	3.8
RNA - localization	6	4.6	RNA - localization	6	4.6
transcription - pol I promoter	5	3.8	transcription - pol I promoter	5	3.8
RNA - poly(A)	3	2.3	RNA - poly(A)	1	0.8
total	130	100.0	total	107	82.3
SIGNALING		%	SIGNALING		%
signaling	46	21.1	signaling	42	19.3
cytokine	28	12.8	cytokine	23	10.6
hormone	20	9.2	hormone	15	6.9
MAPK	17	7.8	MAPK	17	7.8
interferon	16	7.3	interferon	13	6.0
growth factor	12	5.5	growth factor	9	4.1
interleukin	12	5.5	interleukin	9	4.1
Wnt	11	5.0	Wnt	11	5.0
toll-like	8	3.7	toll-like	6	2.8
NFkappaB	7	3.2	NFkappaB	7	3.2
TGF	5	2.3	TGF	5	2.3
Fc	5	2.3	Fc	5	2.3
ERBB	4	1.8	ERBB	4	1.8
insulin	4	1.8	insulin	2	0.9
JNK	4	1.8	JNK	3	1.4
ERK	3	1.4	ERK	3	1.4
JUN	3	1.4	JUN	3	1.4
amine	2	0.9	amine		0.0
TOR	2	0.9	TOR		0.0
chemokine	2	0.9	chemokine		0.0
catenin	1	0.5	catenin	1	0.5
ephrin	1	0.5	ephrin	1	0.5
hippo	1	0.5	hippo		0.0
integrin	1	0.5	integrin		0.0
neurotrophin	1		neurotrophin		0.0
NOD TRK	1	0.5	NOD TRK	1	0.5
IRK	- 1	0.0	STAT	4	1.8
total	218	100.0	total	185	83.0
STRESS		%	STRESS		%
stress	11	19.3	stress	10	17.5
cell death	16	28.1	cell death	9	15.8
response to oxigen	8	14.0	response to oxigen	8	14.0
response to radiation	8	14.0	response to radiation	8	14.0
oxidative stress	12	21.1	oxidative stress	11	19.3
ER - stress	2	3.5	ER - stress	2	3.5
total	57	100.0	total	48	84.2
TRANSPORT		%	TRANSPORT		%
transport	43	32.8	transport	15	11.5
nuclear transport	25	19.1	nuclear transport	19	14.5
endocytosis	13	9.9	endocytosis	8	6.1
exocytosis	12	9.2	exocytosis	6	4.6
vesicle - transport	12	9.2	vesicle - transport	9	6.9
transport of organelles	7	5.3	transport of organelles	7	5.3
transport synaptic	6	4.6	transport synaptic	4	3.1
cytoskeleton - cell projection	5	3.8	cytoskeleton - cell projection	4	3.1
ER - transport	3	2.3	ER - transport	3	2.3
cytoskeleton - based movement	3	2.3	cytoskeleton - based movement	3	2.3
Golgi -vesicle	1	0.8	Golgi -vesicle		0.0
	1	0.8	transport of chromosomes	1	8.0
transport of chromosomes	131	100.0	total	79	60.3
transport of chromosomes		%	WASTE DISPOSAL-QC		%
total					
	34	50.0	ubiquitin-proteasome	30	44.1
total WASTE DISPOSAL-QC ubiquitin-proteasome	34 12			30 10	44.1 14.7
total WASTE DISPOSAL-QC ubiquitin-proteasome autophagy		50.0	autophagy		
total WASTE DISPOSAL-QC ubiquitin-proteasome	12	50.0 17.6		10	14.7
total WASTE DISPOSAL-QC ubiquitin-proteasome autophagy ubiquitin-proteasome - ER UPR	12 7	50.0 17.6 10.3	autophagy ubiquitin-proteasome - ER UPR	10	14.7 10.3
total WASTE DISPOSAL-QC ubiquitin-proteasome autophagy ubiquitin-proteasome - ER UPR cell cycle	12 7 6	50.0 17.6 10.3 8.8	autophagy ubiquitin-proteasome - ER UPR cell cycle	10	14.7 10.3 5.9
total WASTE DISPOSAL-QC ubiquitin-proteasome autophagy ubiquitin-proteasome - ER UPR	12 7 6 4	50.0 17.6 10.3 8.8 5.9	autophagy ubiquitin-proteasome - ER UPR	10 7 4	14.7 10.3 5.9 0.0

ALL GENOME	
semantic class	#
adhesion cell matrix	1
cell cycle	11
cell cycle-cell-proliferation	3
cell cycle - checkpoint	3
cell cycle - phase transition	11
cytoskeleton	1
cell death	14
cell death - intrinsic apoptosis	1
cell death - signaling	3
development	2
NA	
DNA - damage	1
DNA - damage cell death	1
DNA - damage checkpoint	12
DNA - metabolism	3
DNA - repair	1
ER - stress	1
NA	
gene expression	3
protein localization	10
protein localization - membrane	2
protein localization -nucleus	2
response to stimulus - radiation	2
RNA - metabolism	2
signaling	10
signaling - growth factor	2
stress	4
stress - oxidative	2
transcription	2
transcription - pol II promoter	1
translation	1
transport	3
transport - intracellular	13
ubiquitin-proteasome	6
ubiquitin-proteasome - ER	1
UPR	4
TOTAL	139

BRAIN ONLY	
semantic class	#
adhesion cell matrix	1
cell cycle	7
NA	
cell cycle - checkpoint	3
cell cycle - phase transition	11
cytoskeleton	1
cell death	6
cell death - intrinsic apoptosis	1
cell death - signaling	3
development	1
DEVELOPMENT cell-proliferation epithel.	3
DNA - damage	1
DNA - damage cell death	1
DNA - damage checkpoint	11
DNA - metabolism	1
DNA - repair	1
ER - stress	1
gene expres -gene silencing	4
gene expression	3
NA	
protein localization - membrane	2
NA	
response to stimulus - radiation	2
NA	
signaling	9
NA	
stress	4
stress - oxidative	1
NA	
NA	
translation	2
transport	1
transport - intracellular	6
ubiquitin-proteasome	1
ubiquitin-proteasome - ER	1
UPR	4
TOTAL	93

G:PROFILER semantic.group	numb	%a	PANTHER semantic.group	numb.	%o	WEBGESTALT semantic.group	numb	
adhesion adhesion adherens junction	8	4.3	adhesion #	8	5.5	adhesion adhesion adherens junction	4	
adhesion cell cell	6	3.2	adhesion cell cell	5	3.5	adhesion cell cell	3	
adhesion cell matrix adhesion cell substrate	2 5	2.7	adhesion cell matrix adhesion cell substrate	1	0.7	adhesion cell matrix adhesion cell substrate	2	
ageing	5	2.7	ageing	3	2.1	ageing	7	
autophagy	12	6.5	autophagy	7	4.9	autophagy	7	
cell cycle cell cycle-cytoskeleton	20 13	7.0	cell cycle cell cycle-cytoskeleton	5	3.5	cell cycle cell cycle-cytoskeleton	19	
cell cycle - checkpoint	5	2.7	cell cycle - checkpoint	5	3.5	cell cycle - checkpoint	5	
cell cycle - enzyme cell cycle - phase transition	6 26	3.2	cell cycle - enzyme cell cycle - phase transition	20	2.8	cell cycle - enzyme cell cycle - phase transition	4 9	
cell cycle - segregation/cytokinesis	21	11.4	cell cycle - segregation/cytokinesis	14	9.7	cell cycle - segregation/cytokinesis	16	
cell death	34	18.4	cell death	24	16.6	cell death	35	1
cell death - enzymes cell death - ER stress	8	4.3 0.5	cell death - enzymes cell death - ER stress	1	4.9 0.7	cell death - enzymes cell death - ER stress	5	
cell death - extrinsic apoptosis	10	5.4	cell death - extrinsic apoptosis	7	4.9	cell death - extrinsic apoptosis	5	
cell death - intrinsic apoptosis cell death - mitochondria	5	2.7 5.4	cell death - intrinsic apoptosis cell death - mitochondria	5	3.5	cell death - intrinsic apoptosis cell death - mitochondria	5	
cell death - oxidative stress	15	8.1	cell death - oxidative stress	4	2.8	cell death - oxidative stress	1	
cell death - signaling	5	2.7 5.4	cell death - signaling	4	2.8 6.9	cell death - signaling	4	
chromatin cytoskeleton	37	20.0	chromatin cytoskeleton	24	16.6	chromatin cytoskeleton	41	
cytoskeleton - based movement	3	1.6	cytoskeleton - based movement	3	2.1	cytoskeleton - based movement	4	
cytoskeleton - cell projection development	5 115	62.3	cytoskeleton - cell projection development	4 102	2.8 70.7	cytoskeleton - cell projection development	5 144	
development - brain	11	6.0	development - brain	10	6.9	development - brain	11	
development - glia development - neuronal	5	2.7 8.1	development - glia development - neuronal	5	3.5 8.3	development - glia development - neuronal	4	
development - neuronal - axon	8	4.3	development - neuronal - axon	7	4.9	development - neuronal - axon	8	
DEVELOPMENT cell-proliferation EVELOPMENT cell-proliferation epithel.	4	2.2	DEVELOPMENT cell-proliferation	4	2.8	DEVELOPMENT cell-proliferation	4	
DEVELOPMENT cell-proliferation epithel. DEVELOPMENT cell-proliferation stem	5	2.7	DEVELOPMENT cell-proliferation epithel. DEVELOPMENT cell-proliferation stem	4	0.7	DEVELOPMENT cell-proliferation epithel. DEVELOPMENT cell-proliferation stem	8	
DNA - damage	6	3.2	DNA - damage	5	3.5	DNA - damage	6	
DNA - damage cell death	3	1.6	DNA - damage cell death	2	1.4	DNA - damage cell death	2	
DNA - damage checkpoint DNA - metabolism	17	9.2	DNA - damage checkpoint DNA - metabolism	16 21	11.1	DNA - damage checkpoint DNA - metabolism	11 24	
DNA - repair	18	9.7	DNA - repair	12	8.3	DNA - repair	9	
enzyme ER	45	24.4	enzyme ER	40	0.7	enzyme ER	52	
ER - stress	2	1.1	ER - stress	2	1.4	ER - stress	1	
ER - transport	3	1.6	ER - transport	2	1.4	ER - transport	1	
esocytosis gene expres -gene silencing	12 16	6.5 8.7	esocytosis gene expres -gene silencing	9	5.5	esocytosis gene expres -gene silencing	8	
gene expres -transcription factors	6	3.2	gene expres -transcription factors	5	3.5	gene expres -transcription factors	6	
gene expression	7	3.8	gene expression	8	5.5	gene expression	8	
general Golgi	163	88.3 1.6	general Golgi	158	0.7	general Golgi	145	
Golgi -vesicle	1	0.5	Golgi -vesicle	1	0.7	Golgi - vesicle	2	
histone	5	4.3	histone	4	2.8	histone	4	
histone - acetylation histone - methylation	4	2.2	histone - acetylation histone - methylation	2	1.4	histone - acetylation histone - methylation	7	
histone - phosphorylation	2	1.1	histone - phosphorylation	1	0.7	histone - phosphorylation	3	
immune system immune system-chemokine	25	13.5	immune system immune system-chemokine	18	0.7	immune system immune system-chemokine	24	
immune system - antigen presentation	10	5.4	immune system - antigen presentation	10	6.9	immune system - antigen presentation	10	
immune system - differentiation	4	2.2	immune system - differentiation	3	2.1	immune system - differentiation	5	
immune system - innate immune system - leukocytes	7	3.8	immune system - innate immune system - leukocytes	8	5.5 8.3	immune system - innate immune system - leukocytes	8 16	
immune system - lymphocytes	26	14.1	immune system - lymphocytes	14	9.7	immune system - lymphocytes	31	
immune system - receptors	7	3.8	immune system - receptors	7	4.9	immune system - receptors	7	
# localization	29	15.7	localization	27	18.7	ion localization	24	
localization-RNA	1	0.5	localization- RNA	1	0.7	localization- RNA	1	
localization - vesicle	1	0.5	localization - vesicle	1	0.7	localization - vesicle localization golgi	1	
i i						lysosome	1	
membrane	7	3.8	membrane	7	4.9 58.9	membrane	4	
metabolism mitochondria	112	60.6 4.3	metabolism mitochondria	85 5	3.5	metabolism mitochondria	113	
mitochondria - transport	5	2.7	mitochondria - transport	2	1.4	mitochondria - transport	4	
motility muscle	5 35	2.7 18.9	motility muscle	4	2.8	motility muscle	5 32	
nucleus	3	1.6	nucleus	4	2.8	nucleus	3	
organelle	11	6.0	organelle	8	5.5	organelle	10	
organelle - transport phagocytosis	2	0.5	organelle - transport phagocytosis	2	0.7	organelle - transport	2	i
physiology	21	11.4	physiology	22	15.3	physiology	26	ı
protein localization - ER	3	1.6	protein localization - ER	3	2.1	protein localization - cytoskeleton protein localization - ER	2	
protein localization - membrane protein localization - mitochondria	10	5.4	protein localization - membrane protein localization - mitochondria	6 2	1.4	protein localization - membrane	8	
protein localization - mitochonoria protein localization - nucleus	13	7.0	protein localization - mitochondria protein localization - nucleus	6	4.2	protein localization -nucleus	5	
protein modification	27	14.6	protein modification	26	18.0	protein modification	24	
protein modification - acetylation protein modification - alkylation	11	6.0	protein modification - acetylation protein modification - alkylation	6	4.2	protein modification - acetylation protein modification - alkylation	9	
protein modification - aikylation protein modification - folding	3	1.6	protein modification - folding	2	1.4	protein modification - aikylation protein modification - folding	6	
protein modification - neddylation	3	1.6				protein modification - neddylation	3	
protein modification - phosphorylation protein modification - sumoylation	16	1.6	protein modification - phosphorylation protein modification - sumoylation	16 2	11.1	protein modification - phosphorylation protein modification - sumoylation	16	
response to stimulus	76	41.1	response to stimulus	74	51.3	response to stimulus	74	
response to stimulus - oxigen	8	4.8	response to stimulus - oxigen	8	5.5	response to stimulus - oxigen	6	
response to stimulus - radiation RNA - localization	5	4.3	response to stimulus - radiation RNA - localization	8	5.5 3.5	response to stimulus - radiation RNA - localization	8	
RNA - metabolism	30	16.2	RNA - metabolism	25	17.3	RNA - metabolism	23	
RNA - poly(A)	3	1.6				RNA - poly(A)	4	
RNA - spilicing RNA metabolism - stability	12	4.9	RNA - spilicing RNA metabolism - stability	7	2.8	RNA - spilicing RNA metabolism - stability	12	
signaling	46	24.9	signaling	41	28.4	signaling	44	į
signaling - amine signaling - catenin	2	0.5	# signaling - catenin	1	0.7	:		۱
signaling - cytokine		15.2	signaling - cytokine	19	13.2	signaling - cytokine	26	t
	28			1	0.7			
signaling - ephrin	1	0.5	signaling - ephrin			signaling - ERBB signaling - ERK		
signaling - ERBB			signaling - ERBB	3 2	1.4		3 4	
signaling - ERBB signaling - ERK signaling - growth factor	1 4 3 12	0.5 2.2 1.6 6.5		3		signaling - growth factor	4 11	
signaling - ERBB signaling - ERK signaling - growth factor signaling - hippo	1 4 3 12 1	0.5 2.2 1.6 6.5 0.5	signaling - ERBB signaling - ERK signaling - growth factor	3 2 11	1.4 7.6	signaling - growth factor signaling - hippo	4 11 1	
signaling - ERBB signaling - ERK signaling - growth factor signaling - hippo signaling - hormone signaling - insulin	1 4 3 12	0.5 2.2 1.6 6.5	signaling - ERBB signaling - ERK signaling - growth factor signaling - hormone	3 2	1.4	signaling - growth factor signaling - hippo signaling - hormone	4 11	
signaling - ERBB signaling - ERK signaling - growth factor signaling - hippo signaling - hormone signaling - insulin signaling - integrin	1 4 3 12 1 20 4	0.5 2.2 1.6 6.5 0.5 10.8 2.2 0.5	signaling - ERBB signaling - ERK signaling - growth factor # signaling - hormone signaling - insulin #	3 2 11 13 3	1.4 7.6 9.0 2.1	signaling - growth factor signaling - hippo signaling - hormone signaling - insulin signaling - integrin	4 11 1 20 7 1	
signaling - ERBB signaling - ERK signaling - growth factor signaling - hippo signaling - hormone signaling - insulin signaling - integrin signaling - integrin	1 4 3 12 1 20 4	0.5 2.2 1.6 6.5 0.5 10.8 2.2	signaling - ERBB signaling - ERK signaling - growth factor signaling - hormone signaling - insulin signaling - interferon	3 2 11	1.4 7.6 9.0	signaling - growth factor signaling - hippo signaling - hormone signaling - insulin signaling - integrin signaling - interferon	4 11 1 20 7	
signaling - ERBB signaling - ERK signaling - growth factor signaling - prowth factor signaling - hormone signaling - hormone signaling - integrin signaling - integrin signaling - interferon signaling - interferon signaling - INK	1 4 3 12 1 20 4 1 16 12 4	0.5 2.2 1.6 6.5 0.5 10.8 2.2 0.5 8.7 6.5 2.2	signaling - ERB signaling - ERB signaling - ERK signaling - Browth factor signaling - proveth factor signaling - insulin signaling - interferon signaling - interferon signaling - interferon signaling - iNK	3 2 11 13 3 5 5 4	1.4 7.6 9.0 2.1 3.5 3.5 2.8	signaling - growth factor signaling - hippo signaling - hormone signaling - insulin signaling - integrin signaling - interferon signaling - interferokin signaling - JNK	4 11 1 20 7 1 24 29 4	
signaling - ERBB signaling - ERK signaling - growth factor signaling - hippo signaling - hormone signaling - integrin signaling - integrin signaling - interfeukin signaling - interfeukin signaling - MAPK signaling - MAPK	1 4 3 12 1 20 4 1 16 12 4 17	0.5 2.2 1.6 6.5 0.5 10.8 2.2 0.5 8.7 6.5 2.2 9.2	signaling - ERBB signaling - ERK signaling - growth factor signaling - hormone signaling - insulin signaling - interferon signaling - interfeukin	3 2 11 13 3	1.4 7.6 9.0 2.1 3.5 3.5	signaling - growth factor signaling - hippo signaling - hormone signaling - insulin signaling - integrin signaling - interferon signaling - interfevolin	4 11 20 7 1 24 29	
signaling - ERBB signaling - ERK signaling - growth factor signaling - prowth factor signaling - hormone signaling - hormone signaling - integrin signaling - integrin signaling - interferon signaling - interferon signaling - INK	1 4 3 12 1 20 4 1 16 12 4	0.5 2.2 1.6 6.5 0.5 10.8 2.2 0.5 8.7 6.5 2.2 9.2 0.5 3.8	signaling - ERB signaling - ERB signaling - ERK signaling - Browth factor signaling - proveth factor signaling - insulin signaling - interferon signaling - interferon signaling - interferon signaling - iNK	3 2 11 13 3 5 5 4	1.4 7.6 9.0 2.1 3.5 3.5 2.8	signaling - growth factor signaling - hippo signaling - hormone signaling - insulin signaling - integrin signaling - interferon signaling - interferokin signaling - JNK	4 11 1 20 7 1 24 29 4	
signaling - ERBB signaling - BRC signaling - growth factor signaling - hopo signaling - hormone signaling - insulin signaling - instefron signaling - instefron signaling - MAPK signaling - MAPK signaling - MAPK signaling - MAPK signaling - MAPK signaling - MAPK signaling - NEVappBB signaling - NEVappBB signaling - NEVappBB	1 4 3 12 1 20 4 1 16 12 4 17	0.5 2.2 1.6 6.5 0.5 10.8 2.2 0.5 8.7 6.5 2.2 9.2	signaling - URBB signaling - BKR signaling - BKR signaling - BCKR signaling - BCMR signaling - BCMR signaling - BCMR signaling - Interferion signaling - Interferion signaling - INTERPRISE - INTERPRISE signaling - NNA signa	3 2 11 13 3 5 5 4 13	9.0 2.1 3.5 3.5 2.8 9.0	signaling - growth factor signaling - hispop signaling - hormone signaling - instellen signaling - interferen signaling - interferen signaling - interferen signaling - JAK signaling - MAPK signaling - NFAppaB signaling - NFAppaB signaling - NOO	4 11 1 20 7 1 24 29 4 15	
signaling - ERBB signaling - ERK signaling - growth factor signaling - hopo signaling - hormone signaling - integration signaling - integration signaling - integration signaling - AVEX signaling - AVEX signaling - NOD signaling - NOD	1 4 3 12 1 20 4 1 16 12 4 17 1 7	0.5 2.2 1.6 6.5 0.5 10.8 2.2 0.5 8.7 6.5 2.2 9.2 0.5 3.8	signaling - CREB signaling - ERK signaling - proveh factor signaling - hormone signaling - interferon signaling - interferon signaling - interferon signaling - NK signaling - NK signaling - NAK signaling - NAK signaling - NAK	3 2 11 13 3 5 5 4 13	1.4 7.6 9.0 2.1 3.5 3.5 2.8 9.0 4.9	signaling, growth factor signaling,—hippo signaling—hormone stagnaling—instalin signaling	4 11 1 20 7 1 24 29 4 15	
signaling - ERBB signaling - ERK signaling - growth factor signaling - hoppo signaling - hormone signaling - integrin signaling - integrin signaling - integrin signaling - interfectation signaling - MAPK signaling - NAPK signaling - neurotrophin signaling - NAPK signaling - NAPK signaling - NAPK signaling - NAPK signaling - NAPK signaling - NOD	1 4 3 12 1 20 4 1 16 12 4 17 1 7 1	0.5 2.2 1.6 6.5 0.5 10.8 2.2 0.5 8.7 6.5 2.2 9.2 0.5 3.8 0.5	signaling - (ERIB signaling - (ERIR signaling - (ERIX signaling -	3 2 11 13 3 5 5 4 13 7 1	1.4 7.6 9.0 2.1 3.5 3.5 2.8 9.0 4.9 0.7	signaling growth factor signaling. In-pipo signaling - hormone signaling - instelling signaling - instelling signaling - instelling signaling - instelling signaling - instelling signaling - MADPA signaling - MADPA signaling - NOO signaling - NOO	4 11 1 20 7 1 24 29 4 15 8 4 1 1	
signaling - ERBB stgmaling - ERR signaling - growth factor segaling - Rippor signaling - Intuition signaling - Integrin signaling - Interferon signaling - Interferon signaling - Interferon signaling - RNC signaling - RNC signaling - RNC signaling - NOO signaling - NOO signaling - NOO signaling - NOO signaling - TOO signaling - TOO	1 4 3 12 1 20 4 1 16 12 4 17 1 7 1	0.5 2.2 1.6 6.5 0.5 10.8 2.2 0.5 8.7 6.5 2.2 9.2 0.5 3.8 0.5	signaling - ERBB signaling - ERBC signaling - ERCC signaling - ERCC signaling - Smullin signaling - Smullin signaling - Interferon signaling - Interferon signaling - Interferon signaling - INC signaling - TOF	3 2 11 13 3 5 5 4 13	1.4 7.6 9.0 2.1 3.5 3.5 2.8 9.0 4.9 0.7	signaling growth factor signaling. Impop signaling - homone signaling - insulin signaling - insterience signaling - insterience signaling - insterience signaling - NAC signaling - NAC signaling - NAC signaling - NAC signaling - NAC signaling - NAC signaling - INS signaling - INS signal	4 11 1 20 7 1 24 29 4 15 8 4 1 1 4	
signaling - ERBB signaling - ERK signaling - growth factor signaling - hoppo signaling - hormone signaling - integrin signaling - integrin signaling - integrin signaling - interfectation signaling - MAPK signaling - NAPK signaling - neurotrophin signaling - NAPK signaling - NAPK signaling - NAPK signaling - NAPK signaling - NAPK signaling - NOD	1 4 3 12 1 20 4 1 16 12 4 17 1 7 1	0.5 2.2 1.6 6.5 0.5 10.8 2.2 0.5 8.7 6.5 2.2 9.2 0.5 3.8 0.5	signaling - (ERIB signaling - (ERIR signaling - (ERIX signaling -	3 2 11 13 3 5 5 4 13 7 1	1.4 7.6 9.0 2.1 3.5 3.5 2.8 9.0 4.9 0.7	signaling growth factor signaling. In-pipo signaling - hormone signaling - instelling signaling - instelling signaling - instelling signaling - instelling signaling - instelling signaling - MADPA signaling - MADPA signaling - NOO signaling - NOO	4 11 1 20 7 1 24 29 4 15 8 4 1 1	
signaling - ERBB signaling - ERR signaling - growth factor signaling - hopo signaling - hopo signaling - hormone signaling - integrin signaling - integrin signaling - integrin signaling - interleukin signaling - interleukin signaling - PRE signaling - PRE signaling - NOD ### signaling - NOD ### signaling - TOS	1 4 3 12 1 20 4 1 16 12 4 17 7 1 7 1	0.5 2.2 1.6 6.5 0.5 10.8 2.2 0.5 8.7 6.5 2.2 9.2 0.5 3.8 0.5	signaling - ERBB signaling - BKK signaling - BKK signaling - BKK signaling - Pownhole signaling - Internet signaling - TOP signal	3 2 11 13 3 5 5 4 13 7 1	1.4 7.6 9.0 2.1 3.5 3.5 2.8 9.0 4.9 0.7 3.5 2.8	signaling growth factor signaling. Inpop signaling - hormone signaling - insulin signaling - insulin signaling - insteprin signaling - insteprin signaling - insuling - i	4 11 1 20 7 1 24 29 4 15 8 4 1 1 4 12 3	
signaling - ERBB signaling - ERC signaling - growth factor signaling - hopo signaling - hormone signaling - hormone signaling - interferon signaling - interferon signaling - interferon signaling - NAPK signaling - NAPK signaling - NAPK signaling - NAPK signaling - NAPK signaling - TOS signaling - TOS	1 4 3 12 1 20 4 1 16 12 4 17 1 7 1 7 1 5 8 2 2 1 1 1 5 1 5 1 1 7 1 1 7 1 1 7 1 1 7 1 1 7 1 1 7 1 1 7 1	0.5 2.2 1.6 6.5 0.5 10.8 2.2 0.5 8.7 6.5 2.2 9.2 0.5 3.8 0.5	signaling - (ERIB signaling - (ERIR signaling - (Interfection signaling - (Interfection signaling - (Interfection signaling - (ERIR signal	3 2 11 13 3 5 5 4 13 7 1	1.4 7.6 9.0 2.1 3.5 3.5 2.8 9.0 4.9 0.7 3.5 2.8	signaling growth factor signaling. Appop signaling - hormone signaling - hormone signaling - insulin signaling - insulin signaling - insuling - insu	4 11 1 20 7 1 24 29 4 15 8 4 1 1 1 4 12 3 3 1 7	
signaling - ERBB signaling - BRC signaling - Browth factor signaling - Independent - Independent signaling - Independent - Independent signaling - Interferon signaling - Interferon signaling - Interferokan signaling - DRC signaling - SRC signaling - SRC signaling - SRC signaling - Independent - Independent signaling - TOS signaling - TOS	1 4 3 12 1 20 4 1 16 12 4 17 7 1 7 1	0.5 2.2 1.6 6.5 0.5 10.8 2.2 0.5 8.7 6.5 2.2 9.2 0.5 3.8 0.5	signaling - ERBB signaling - BKK signaling - BKK signaling - BKK signaling - Pownhole signaling - Internet signaling - TOP signal	3 2 11 13 3 5 5 4 13 7 1	1.4 7.6 9.0 2.1 3.5 3.5 2.8 9.0 4.9 0.7 3.5 2.8	signaling growth factor signaling. Impop signaling - homone signaling - insulin signaling - instantion signaling - instantion signaling - instantion signaling - NAC signaling - COL signaling - TOL signaling - TOL signaling - TOL signaling - TOL signaling - TOL signaling - TOL signaling - TOL	4 11 1 20 7 1 24 29 4 15 8 4 1 1 4 12 3 1	
signaling - ERBB signaling - ERBC signaling - ERBC signaling - ERBC signaling - Hope signaling - International signaling - Internation signaling - Interferon signaling - Interferon signaling - Interferon signaling - NAC signaling - NAC signaling - NAC signaling - NAC signaling - NAC signaling - TOS signaling - TOS si	1 4 3 122 1 200 4 4 1 16 12 4 4 17 7 1 5 8 2 1 11 5 3 11 12	0.5 2.2 1.6 6.5 0.5 10.8 2.2 9.2 9.2 0.5 3.8 0.5 2.7 4.3 1.1 0.5 6.0 2.7 4.3 1.1 0.5 6.0 6.5 6.5 6.5 6.5 6.5 6.5 6.5 6.5 6.5 6.5	signaling - ERBB signaling - ERBC signaling - ERCC signaling - ERCC signaling - ERCC signaling - ERCC signaling - Interferon signaling - Interferon signaling - Interferon signaling - INC signaling - INC signaling - INC signaling - INC signaling - TOF signaling - IVE sig	3 2 11 13 3 5 5 4 4 13 7 1 1 5 4	1.4 7.6 9.0 2.1 3.5 3.5 2.8 9.0 4.9 0.7 3.5 2.8 3.5 2.8 9.0 7.6 3.5 2.8 7.6 3.5 2.8	signaling growth factor signaling. Impop signaling in homone signaling installar signaling installar signaling signalin	4 11 1 20 7 1 1 24 29 4 15 8 4 1 1 1 4 1 2 3 1 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	
signaling - ERBB signaling - ERBB signaling - Brown factor signaling - Incover factor signaling - Incover factor signaling - Incover factor signaling - Incover factor signaling - Integration signaling - Integration signaling - Integration signaling - Interfeciability signaling - Into I-like signaling - Into I-l	1 4 3 12 1 200 4 1 16 12 4 17 1 7 1 1 15 5 8 2 1 11 15 5 3 111 12 2	0.5 2.2 1.6 6.5 0.5 8.7 6.5 2.2 9.2 9.2 0.5 3.8 0.5 2.7 4.3 1.1 0.5 6.0 2.7 1.6 6.0 6.0 6.0 6.0 6.0 6.0 6.0 6.0 6.0 6	signaling - CRBB signaling - ERK signaling - Normone signaling - Interferon signaling - Interferon signaling - Normone signaling - Toll sign	3 2 11 13 3 5 5 5 4 13 7 7 1	1.4 7.6 9.0 2.1 3.5 3.5 2.8 9.0 4.9 0.7 3.5 2.8 7.6 3.5 2.1 5.5 5.5 2.8	signaling growth factor signaling. Apppo signaling - hormone signaling - incurin signaling - incurin signaling - integrin signaling - integrin signaling - integrin signaling - integring - integraling - in	4 11 1 20 7 1 1 24 29 4 15 8 4 1 1 1 4 12 3 1 7 7	
signaling - ERBB signaling - ERBC signaling - ERBC signaling - ERBC signaling - Hope signaling - International signaling - Internation signaling - Interferon signaling - Interferon signaling - Interferon signaling - NAC signaling - NAC signaling - NAC signaling - NAC signaling - NAC signaling - TOS signaling - TOS si	1 4 3 122 1 200 4 4 1 16 12 4 4 17 7 1 5 8 2 1 11 5 3 11 12	0.5 2.2 1.6 6.5 0.5 10.8 2.2 9.2 9.2 0.5 3.8 0.5 2.7 4.3 1.1 0.5 6.0 2.7 4.3 1.1 0.5 6.0 6.5 6.5 6.5 6.5 6.5 6.5 6.5 6.5 6.5 6.5	signaling - (ERIB signaling - (ERIR signaling -	3 2 2 11 13 3 3 5 5 4 13 7 7 1 11 5 3 8 8 11 2 1 1 6	1.4 7.6 9.0 2.1 3.5 3.5 2.8 9.0 4.9 0.7 3.5 2.8 3.5 2.8 4.9 0.7	signaling growth factor signaling. Appop signaling - hormone signaling - incurin signaling - incurin signaling - integrin signaling - integrin signaling - NAD signaling - NAD signaling - NAD signaling - NAD signaling - NOO signaling - NOO signaling - NOO signaling - NOO signaling - TOO signaling	4 11 1 20 7 1 24 29 4 15 8 8 4 1 1 1 4 12 3 1 7 7	
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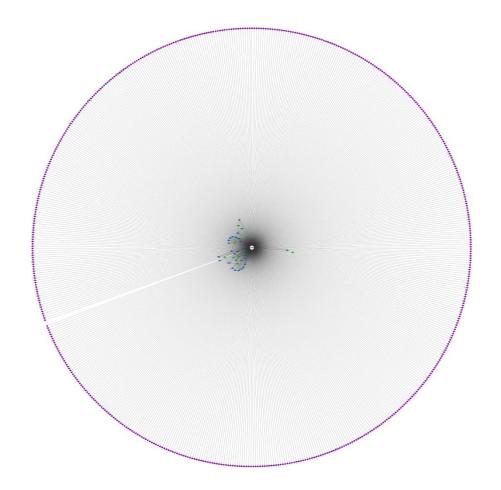
FTD - 29 IIHs			ALBINISM - 79 proteins		
semantic.group	numb.	%0	semantic.group	numb.	%
adhesion cell matrix	1	3.7			
cell cycle	11	40.6	#		
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cell cycle-cell-proliferation	3	11.1			
cell death	14	51.7	#		
cell death - intrinsic apoptosis	1	3.7	#		
cell death - signaling	3	11.1	#		
development	2	7.4	#		
DNA - damage	1	3.7	#		
DNA - damage cell death	1	3.7	#		
DNA - damage checkpoint	12	44.3	#		
DNA - metabolism	3	11.1	#		
DNA - repair	1	3.7	#		
#			endocytosis	1	22.
enzyme	4	14.8	enzyme	1	22.
gene expression	3	11.1	#		
general	60	221.4	general	7	159.
metabolism	31	114.4	metabolism	1	22.
mitochondria	1	3.7	#	17	
organelle	2	7.4	#		
#			pigment	10	227
physiology	1	3.7	#		
protein localization	10	36.9	protein localization	1	22.
protein localization - membrane	2	7.4	#		100
protein localization -nucleus	2	7.4	#		
protein modification	14	51.7	#		
protein modification - folding	1	3.7	#		
protein modification - phosphorylation	4	14.8	#		
response to stimulus	13	48.0	response to stimulus	6	136.
response to stimulus - radiation	2	7.4	#	0	100.
RNA - metabolism	2	7.4	#		
signaling	10	36.9	signaling	8	181.
signaling - growth factor	2	7.4	#	0	101.
stress	4	14.8	#		
stress - oxidative	2	7.4	#		
stress - ER	1	3.7	#		
	2	7.4	#		
transcription	1	3.7	#		
transcription - pol II promoter	1	3.7	#		
translation	3	11.1		2	45.
transport		40000000	transport	2	
transport - intracellular	13	48.0	transport - intracellular	6	136.
ubiquitin-proteasome	6	22.1	#		
ubiquitin-proteasome - ER	1	3.7	#		00
#	04	440	vesicle - transport	1	22.
UPR	4	14.8	#		
virus	2	7.4	#		
120212			92 2002	7.35	
total	271		total	44	

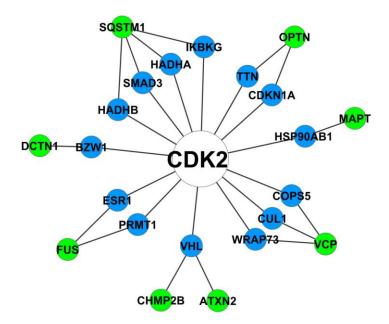
GO:004	2440	pigment metabolic process
GO:000	6582	melanin metabolic process
GO:004	3474	pigment metabolic process involved in pigmentation
GO:004	8066	developmental pigmentation
GO:004	3324	pigment metabolic process involved in developmental pigmentation
GO:004	8069	eye pigmentation
GO:004	2441	eye pigment metabolic process
GO:004	6148	pigment biosynthetic process
GO:000	6726	eye pigment biosynthetic process
GO:004	2438	melanin biosynthetic process

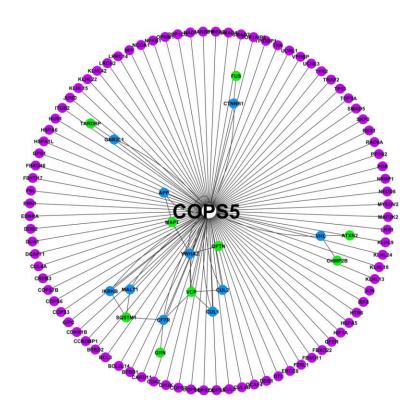
4.84E-65 1.23E-06	154 50	4132 4132	71	0.019	0.402	0.0007160 cell-metris adhesion 0.0000902 regulation of cell-metris adhesion	5 oil-natis 5 oil-natis	cell matrix adhesion 78 unique proteira
2.800-00	340 84	4132 4132 4132	111 45	0.032 0.011 0.011	0.383 0.536 0.529	2 0000615 represent set professione 0 0006155 requirement of the extent profession 0 0006145 requirement of the extent profession 0 0006145 strategies and profession of professional 0 00061466 securities regulation of filterations and filtration	4 self-proliferation 5 self-proliferation 4 cell-proliferation	
2.72E-66 2.72E-66 8.66E-60	85 292 52	4152 4152 4152	45 108 27	0.011 0.026 0.007	0.529 0.383 0.529	0.0048144 fibroblest proliferation 0.0000078 regulation of epithetial cell proliferation 0.0048146 popular regulation of fibroblest proliferation	4 cell-proliferation 5 cell-proliferation 6 cell-proliferation	epithelial cell proliferation 165-unique proteins
2.126-12 1.056-30 1.026-19	662 369 121	4352	274 261	0.066	0.449 0.447	0.0070888 response to growth factor	5 signaling growth factor 6 signaling growth factor	
1.005-19	121	4352 4352	48	0.019	0.645	0.007868 impanse to govern fector 0.0071555 cellular response to govern fector dimulsa 0.0071555 cellular response to govern fector dimulsa 0.0001111 posternosa govern fector resolutor organiza pathway 0.0002006 regolutor el delibernosi govern fector resolutor signale signale 0.0002006 regolutor regulation of epidemiai govern fector resolutor 0.0002006 regolutor regulation of epidemiai govern fector resolutor	9 signaling - growth factor 7 signaling - growth factor	
1.645-05	45	4152	12	0.008	0.765		6 signaling - growth factor 2 signaling - growth factor	growth factor signaling
3.73E-09 3.5EE-00 4.29E-06 4.45E-05	92 35 27	4152 4152	23	0.006	0.742 0.739 0.43	OROROWS usuade endothelist gloot feeler receptor organists perhans 1007/2000 reasons to explained goods feeler portratted enlare requirement organism and goods feeler 1005/2006 feeler requirement organism appeals feeler 1005/2006 feeler goods feeler requirement general general 1005/2006 gloots requirement in feeler general general general 1005/2006 gloots requirement of feeler general general general 1005/2006 gloots gloots and ordains requirement general general general	4 signaling growth factor 7 signaling growth factor 8 signaling growth factor 7 signaling growth factor 4 signaling growth factor 4 signaling growth factor	365 unique protecra
	157 133 139	4152 4152 4152 4152 4152	46 34 55	0.006 0.005 0.011 0.013	0.43 0.400 0.396 0.204	0 (000545 fibroblest growth factor receptor signaling perhine) 0 (004594) certular response to fibroblest growth factor stimulus 0 (007) 778, response to fibroblest growth factor	8 signating growth factor 7 signating growth factor 4 sensiting arouth factor	
1.47E-E2	226	4137	10	0.013	0.334	0.0090287 regulation of calcular response to growth factor attivable	4 signating - growth factor	
7.266-77 2.036-76 1.04E-41	400 268	4352 4352 4352	313 302 175	0.075 0.073 0.042	0.638 0.608	20000001 general and the segment general segment general segments general	4 phase transition 5 phase transition 6 phase transition 6 phase transition	
9.87E-13 3.75E-13	150 139	4152	\$46 79	0.042 0.044 0.02 0.019 0.000 0.007 0.006 0.006	0.589 0.598	D 2900907 regulation of self-cycle phase transition D 2900908 regulation regulation of cell cycle phase transition D 2900995 regulation regulation of reflects cell cycle phase transition.	7 phase transition	mitotic abase trassition
3.756-33 2.862-04 3.566-64 9.146-60	53 54 26	4152 4152	30 30	0.00E 0.007	0.542 0.596 0.494	D 2000000 positive regulation of cell cycle phase transition 0 0000000 assistive regulation of relative cell cycle phase transition 0 00000000 as in from militaria	7 phase transition 7 phase transition 8 phase transition	mitotic phase transition 313 unique proterro
1.665-60	40	4152 4152	24	0.006	0.542 0.542 0.596 0.494 0.545 0.533	O 0000091, metaphage/anaphase transition of witable cell cable O 0004794, metaphase/anaphase transition of cell cycle	7 phase transition 7 phase transition 8 phase transition 9 phase transition 6 phase transition 1 phase transition	
4.031-62	44	4152	23	0.000	0.523	0 0000002 01,7 Nersman of within cell cycle	6 phase transition	
1.738-34 1.756-36	225 229 141 131	4132 4132 4152	344 344 82	0.034 0.035 0.02 0.015 0.013 0.013	0.613 0.582	D 80000002 GL/1 francistion of installic cell cycle D 8044845 cell cycle GL/5 phase transition D 2002866 regulation of cell cycle GL/1 phase transition	6 phase terrotion 5 phase terrotion 7 phase terrotion 7 phase terrotion 8 phase terrotion 8 phase terrotion	
1.546-34 1.738-34 1.156-36 1.256-36 1.636-33 2.366-33	131 90 94	4152 4152	76 33 54	0.015	0.595 0.604 0.596	Upper de la companya del compan	7 phase transition 8 phase transition 7 phase transition 10 phase transition	GI/S phase transition 144 unique proteins
9.14E-E0 1.95E-E0 3.70E-E0	26 27 28	4152 4152 4151	17	0.004	0.69	gyappappag impoletion of harmonication involved in IEUS transition of whitelic cell cycle 0.0000000 profiles regulation of cell cycle IEUS phase harmonical 0.00000000 profiles regulation of IEUS harmonical anilate cell cycle	10 phase transition 8 phase transition 8 phase transition	
3.70E-00 5.89E-27		4152	13	0.004	0.652		phase transition phase transition	
2.354-25 2.866-66 5.366-60	190 181 59	4052 4052 4052	110 32 27	0.026 0.008 0.007	0.542 0.529	0-0046009 cell cycle CLVM phase transition 0-0000006 GLM Sewitton of instruct cell cycle 0-0000709 regional cell cell cell cell cycle 0-0007099 regional cell cell cell cell cell cycle 0-0000099 regional cell GLMM transition of instruct cell cycle	6 phase transition 7 phase transition 7 phase transition	G2/M phase tramition 116-anique proteins
A.56E-27	213	4132	123	0.00	0,387	C (000007) cell cycle checkpoint	4 checkpoint	
5.686-17 5.556-39 3.631-06	65 65	4132 4132	84 44 40	0.02 0.011 0.02	0.579 0.638 0.635	0.0000000 minus cell cycle dedispassi 0.0048031 minus 42.5 seruntur abeckpossi 0.0072305 signal transbutturi inschedi in cell cycle desbyaniti	6 theckpore 5 theckpore 7 checkpore	cell cycle checkpoint 125 unique proteins
1.400-00 1.400-07	62	4152	40 38	0.009	0.613	0.0072305 signel terophotion involved in set syste shebypoint 0.0072433 signel terophotion involved in mitoda cell syste shebypoint	7 chespore 8 chespore 5 chespore	7.10
9.792-23 9.792-23	153 143 115	4152 6152	70	0.022	0,636	0.0000077 SNA-famage checkpoint 0.00000079 SNA-famage response, nigral transduction by p53 class mediator	6 DNA damage dreckpoint 7 DNA damage dreckpoint	
9.45E-19 1.19E-14 1.83E-13	56 92	4132 4152	60 14	0.015 0.014 0.00 0.00 0.009	0.633	mediatur 2004/75 millotic Dah Lintegrits dheckpoine 30004775 millotic Dah dennege dherberine 30007482 signel manded on intollinet in 264 integrits dheckpoine 30007482 signel manded on intollinet in 264 diseage checkpoine 30007482 signel manded to intollinet in 1644 diseage checkpoine 0,000,000 signel handed to intollinet in 1646 (diseage checkpoine	7 DNA damage dheckpoint 8 DNA damage dheckpoint 8 DNA damage dheckpoint 9 DNA damage dheckpoint 9 (INA damage dheckpoint	
LR16-13 1.775-06 1.776-06	64	4152 4152 4252	40	0.00	0.63 0.625 0.625 0.625	D30734EL signal transduction involved in DAA Integrity chackgoint D30734E2 cignal transduction involved in DAA damage chackgoint D3903466 cignal transduction involved in installs DBA integrity	DNA damage disoxporet DNA damage disoxporet DNA damage disoxporet	DNA damage checkpoint 125 unique proteins
1.406-07 1.406-07	62	4152	38	0.009	0.613	O 2900402 ognet transluction incorned in relation DNA dawage checkpoint O 90004577 DNA damage imperior, signet transluction by \$55 closes	10 DNA damage checkpoint 12 DNA damage checkpoint	
1.94E-E7 3.04E-E0	22	4152	18	0.004	0.642	mediator resulting in cell cycle arrist	8 DNA damage checkpoint	
3.666-60	14	4153	11	0.000	0.795	ps3 false mediator 3,00000000 DAN demands response, rignal transduction for \$55 class mediator resulting in transcription of \$55 class mediator mediator resulting in transcription of \$55 class mediator	1 DNA damage checkpoint	
1.931-50 3.556-32	70 03	4352 4352 4352	45 44 38	0.011 0.011 0.000	0.638 0.638 0.623		7 DNA damage checkpoint 10 DNA damage checkpoint 10 DNA damage checkpoint	[MiA damage checkpoint 6: 45 unique proteire
6.90E-08	61	4152	18	0.000	0.623	D 0072431 Infrash harodwitten involved in mitels CI ONA denage checkerse	II DNA famage chackpoint	45 unique proteirs
5.340-37	274 149	4152	343 85	0.039	0.393	0.0007110 minus approids ognating sellives 0.000230 mg/minus el noveso approids sellives	6 cell death intrinsic apophosis 7 cell death intrinsic apophosis	
1.336-36 4.972-08 1.096-07 1.226-07	72	4152 4152 4152	45 34	0.02 0.00 0.006 0.012	0.509 0.654	0.0007180 retrissis appliedis operating pethylegi 0.0001820 inguistion of infrassis aspector, significial pathylesis 0.0001820 retrissis appliedis specting pethylesis politicis medisturi 0.0000240 appliedis pethylesis of infrassis appliedis spectific spectificial pethylesis 0.0000240 applied stigulation of intrinsis appliedistic appliedis pathylesis 0.0000250.	7 cell death - intrinet apoptosis 7 cell death - intrinet apoptosis 7 cell death - intrinet apoptosis 6 cell death - intrinet apoptosis	cell deuth via Intrinsic apopto 165 unique proteins
4.00[-67	93.	4152 4152 4132	329	0.012 0.077 0.05	0.563 0.562	0.0007190 aboutoits signating pathway	6 cell-death - intrinsk-apoptosis 5 cell-death - signaling 6 cell-death - signaling	
2.625-42 5.946-27 3.746-38 3.936-60	568 171 294 9	4152 4152 4152	201 208 208	0.05 0.026 0.026 0.002	0.562 0.529	0.002150 Apostoric signaling pathwas 0.000233 registron of apostoric opening pathwas 0.000230 postoric registron of apostoric signaling pathwas 0.000234 register registron of excepts; specing pathwas 0.000234 register register of excepts; specing pathwas 0.000200 death-infacing signaling complic assentity	e cell-death signaling 6 cell-death signaling 5 cell-death signaling 7 cell-death signaling	apoptotic signaling 215 unique proteins
7.506-14	101	4132	60	0.015	0,612		7 DNA - damage cell death	
1.982-05	42	4152	29 21	0.007	0.643	\$1,000,000 occasion of occasion appetitude significant or operator to UNA. \$1,000,000 occasion of occasion appetitude significant to UNA. \$1,000,000 occasion of occasion appetitude.	8 ENA - damage cell death 8 ENA - damage cell death	Intrinsic apoptosis after DNA da 63 unique proteins
2.546-68 2.846-59 3.036-23	764	4152 4132		0.090	0.493	to ONA-develope 0.0000974 celtular response to DNA-develope streams	90 - 000 - 000 0 Parking 190 00	
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1,775-88 1,286-60 9,475-68	51 55 36	4152 4152	28 25	0.007 0.007 0.005	0.549	0.000001 regative regulation of response to DAR damage stimulus 0.0042769 DBA damage response, detection of DBA damage	4 DNA-datage 6 DNA-datage	i competendenco
6.886-28 1.436-34 7.456-33 9.296-00	467 135	4152 4152	227 68	0.055	0.457	Control of the American State of the America	6 DNA-repair 7 DNA-repair	
7.49E-13 9.29E-EE 3.4EE-E7	70 74 29	4152 4152 4152	48 41 21	0.016 0.012 0.01 0.006 0.019 0.006 0.006 0.006	0.402 0.408 6.581 6.793 6.417 0.729 0.729	0.0000263 transprigition oraginal exclusivide excision regain 0.0000262 regulation of DNA report 0.0000294 inscharing excision repair, preincipies complex essentity	F UNA report T UNA report E UNA report	
3.400-07 4.550-06 9.790-06	192 32	4152 4152	25 18	0.006	8.417 9.729 0.739	0.0000002 duuliestrand brokingair 0.0000011 globel genove nucleatide esclaior repeir	7 DNA repair 8 DNA repair	
3.69E-E5 3.69E-E0	21	4132 4132	17	0.004	15.0	0.0000250 inucleotide exclusion repair, 294 inclusion, 3º fai lesion 0.0000250 inucleotide exclusion repair, previolate complex stabilisation.	3 Disk cooper	044 denuge repair 227 urrique proteiro
0.45E-66 1.59E-60 3.52E-60	22 22	4152 4152 4152 4152 4152	25 16 22	0.006	0.622 0.727 0.595	0.0040739 assiste regulation of 044 repair 0.0000717 nucleotide-excision repair, DNA duples arranding 0.0000296 nucleotide-excision repair, DNA incipion, V-to lector	5 DNA-repair 5 DNA-repair 5 DNA-repair	
3.83E-E5 3.70E-E0 0.04E-E0	55 79 20	4152 4152	28 25	0.007	0.538 0.429 0.423	D (0006SEL postrepilication repeir D (0006SEL Sett synthesis involved in DNA repeir D (0006SEL	7 DNA repair 7 DNA repair 2 DNA repair	
6.456-66 1.596-60 3.536-60 3.836-60 1.706-60 8.046-60 1.156-60	35	4132 4152	22 21	0.006 0.004 0.005 0.007 0.008 0.008 0.008 0.005	0.538 0.479 0.472 0.364 0.477	3 DIASTER SINGHAM ENGINEERING AND	B DNA reguler 5 DNA reguler 5 DNA reguler 7 DNA reguler 7 DNA reguler 7 DNA reguler 7 DNA reguler 8 DNA reguler 8 DNA reguler 8 DNA reguler 8 DNA reguler	
1.010-24	422 124	4152 4152	194 75	0.047	0.463	D 90000014 response to redistrion	4 response to stimulus - rediction	
1.826-36 1.300-34 2.576-08 3.338-07	124 141 158	4152 4152	79	0.018 0.019 0.018	0.905 0.30 0.463	0:0009611 response to UV 0:0000012 response to inviving radiation 0:00000130 ortical response to radiation	6 response to stimulus - radiation 3 response to stimulus - radiation 5 response to stimulus - radiation 7 response to stimulus - radiation	response to lending radiatio
2.08E-06 3.631-06 7.99E-00	56 56 32	4132 4132 4132 4132	34 31	0.008 0.008 0.007 0.005	0.463 0.554 0.607 0.62 0.605	00074670 certular response to rediction 00030668 startular response to rediction 00030687 estimate response to the control rediction 0003052 response to promote serior rediction 0003052 response to annex serior ce	5 response to stimulus - radiation 7 response to stimulus - radiation 6 response to stimulus - radiation 6 response to stimulus - radiation 6 response to stimulus - radiation	
	222	4152	112	0.027	0.531	0.0034059 cellular response to oxidative stress	5 stress-condutive	
		4152	147 73 103		0.448 0.698 0.507 0.503	0.0042542 response to hydrogen perovide	6 Stress - cuidative 6 Stress - cuidative 5 stress - cuidative 6 Stress - cuidative	
5.09E-39 9.61E-19 3.54E-38 L85E-35	375 120 203		68	0.016	0.553	0.0034634 cellular response to tractive seagen species 0.0078361, cellular response to hydrogen perceide	6 Stress - cuidative 7 stress - cuidative	
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9.631-19 5.542-28 1.696-15 6.277-32 1.996-28 1.996-28 1.996-69 7.996-69 7.996-69 7.996-69 3.166-69 3.1	74 56 56 56 56 56 56 56 56 56 56 56 56 56	4152 4152 4152 4153 4152 4152 4152 4152 4152 4152 4153 4153 4153 4153 4153 4153 4153 4153	148 28 42 43 50 22 5 11 13 94 18 75 67 11	0.036 0.006 0.013 0.014 0.000 0.000 0.000 0.000 0.002 0.024	0.579 0.409 0.762 0.762 0.603 1 0.646 0.633 0.534 0.534 0.534 0.535 0.547 0.547 0.547	Section Section of Section 2 and Section 2 a	1	IR stress 148-strope proteins 158-strope proteins 1113-strope proteins 1113-strope proteins
9.011-19 1.001-19 1.0	76 56 60 22 22 22 25 16 256 26 26 27 27 27 27 27 27 27 27 27 27 27 27 27	4152 4152 4152 4153 4152 4152 4152 4152 4152 4152 4153 4153 4153 4153 4153 4153 4153 4153	148 28 42 49 16 22 9 11 33 94 18 75 67	0.036 0.000 0.013 0.013 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000	0.579 0.409 0.762 0.762 0.603 1 0.646 0.633 0.534 0.534 0.534 0.535 0.547 0.547 0.547	Section Section of Section 2 and Section 2 a	1	Di direa 141-yespe protein 151-shippin proteine 151-shippin proteine 151-shippin proteine 151-shippin proteine 151-shippin proteine 151-shippin proteine
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0.011 in 0.0	76 (6) (7) (8) (8) (8) (8) (8) (8) (8) (8) (8) (8	4153 4152 4152 4153 4153 4153 4153 4153 4153 4153 4153	244 25 25 25 25 25 25 25 25 25 25 25 25 25	0.036 0.035 0.031 0.031 0.031 0.030 0.000	6.539 6.964 6.762 6.362 6.863 1 6.863 1 6.863 6.553 6.967 6.9	Section Section of Section 2 and Section 2 a		ER divine 148-y-incipe proteins 88 shippile parkanere 1113-reque proteins UNI 38 sreque proteins CR transport 29 sreque proteins
0.011 in 0.0	76 59 59 59 59 59 59 59 5	4155 4105 4105 4105 4105 4105 4105 4105	244 25 25 25 25 25 25 25 25 25 25 25 25 25	0.036 0.035 0.031 0.031 0.031 0.030 0.000	6.539 6.964 6.762 6.362 6.863 1 6.863 1 6.863 6.553 6.967 6.9	Section Section of Section 2 and Section 2 a		Microse Microse protects
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9.031-31 (1992) 5.356-23 (1992) 6.279-12 (1992	76 56 56 56 56 56 56 56	4137 4137 4137 4137 4137 4137 4137 4137	284 28 48 66 62 22 3 3 11 12 12 12 12 12 12 12 12 12 12 12 12	0.036 0.000 0.011 0.0000 0.000	0.578 0.698 0.576 0.762 0.762 0.698 0.698 0.502 0.602 0.602 0.603 0.602 0.503 0.502 0.602 0.603 0.602	Selection of the control of the cont	The control of t	Microse Memory application of the Control of the Co
9-031-31 Section 2-1 Section 2	76 56 56 56 56 56 56 56	4132 4132 4132 4133 4133 4133 4133 4133	244 28 22 49 40 40 40 40 40 40 40 40 40 40 40 40 40	0.006 0.006 0.006 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0	0.578 0.6694 0.767 0.762 0.522 0.625	Section Section of Section 1 and Section 1 a	A control cont	Microse Memory application of the Control of the Co
9-031-31 Section 2-1 Section 2	76 56 56 56 56 56 56 56	4132 4132 4132 4133 4133 4133 4133 4133	244 25 22 22 23 25 24 25 25 25 25 25 25 25 25 25 25 25 25 25	0.006 0.006 0.006 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0	0.578 0.6694 0.767 0.762 0.522 0.625	Section Section of Section 1 and Section 1 a	A control cont	18 days 38 wased partners 18 shipping partners 18 shipping partners 18 wased partners 18 wased partners 18 wased partners 29 wased partners 20 wased partners
9-031-31 Section 2-1 Section 2	76 56 56 56 56 56 56 56	4132 4132 4132 4133 4133 4133 4133 4133	248 26 26 27 27 27 27 27 27 27 27 27 27 27 27 27	0.006 0.006 0.006 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0	0.578 0.6694 0.767 0.762 0.522 0.625	Section Section of Section 1 and Section 1 a	1	Microse Microse protects
6-041-13 (1996) 6-107-12 (1996	76 56 56 56 56 56 56 56	4133 4132 4132 4132 4133 4133 4133 4133	144 24 24 24 24 24 24 24 24 24 24 24 24 2	8.036 8.006 9.011 9.012 9.012 9.000	6.579 0.009 0.747 0.757 0.009 0.009 0.747 0.757 0.750 0.009 0.750	Section Section of Section 2 and Section 2 a	1	Microse Microse protect Microse protec
6-041-13 (1996) 6-107-12 (1996	76 56 56 56 56 56 56 56	4153 4132 4132 4132 4132 4132 4132 4132 413	144 24 24 24 24 24 24 24 24 24 24 24 24 2	8.036 8.006 9.011 9.012 9.012 9.000	6.579 0.009 0.747 0.757 0.009 0.009 0.747 0.757 0.750 0.009 0.750	Section Section of Section 2 and Section 2 a	A control cont	Microse Microse protect Microse protec
6-041-13 (1996) 6-107-12 (1996	76 56 56 56 56 56 56 56	4153 4132 4132 4132 4132 4132 4132 4132 413	144 24 24 24 24 24 24 24 24 24 24 24 24 2	8.036 8.006 9.011 9.011 9.010 9.000	6.579 0.009 0.747 0.757 0.009 0.009 0.747 0.757 0.750 0.009 0.750	Section Section of Section 2 and Section 2 a	A control cont	IN COMM 25 COMMAND AND ADMINISTRATION OF THE
6.004 1.005	78	4133 4132 4132 4132 4133 4133 4133 4133	248 26 26 27 27 27 27 27 27 27 27 27 27 27 27 27	8.036 8.006 9.011 9.011 9.010 9.000	6.579 0.009 0.747 0.757 0.009 0.009 0.747 0.757 0.750 0.009 0.750	Section Section of Section 2 and Section 2 a	A	Microse Microse protect Microse protec
9-031-31 Section 2-1 Section 2	76 76 76 76 76 76 76 76	4153 4132 4132 4132 4132 4132 4132 4132 413	144 24 24 24 24 24 24 24 24 24 24 24 24 2	8.036 8.006 9.011 9.012 9.012 9.000	6.579 0.009 0.747 0.757 0.009 0.009 0.747 0.757 0.750 0.009 0.750	Section Section of Section 2 and Section 2 a	A	IN COMM 25 COMMAND AND ADMINISTRATION OF THE
6.054 13 13 13 13 13 13 13 1	76 76 76 76 76 76 76 76	4633 4633 4633 4633 4633 4633 4633 4633	144 28 46 46 46 46 46 46 46 46 46 46 46 46 46	0.036 0.000 0.001 0.0000 0.00000 0.00000 0.00000 0.000000	6.539 6.609 6.707	Selection of the control of the cont	A control cont	18 depend protects 18 depends
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6.002 10 10 10 10 10 10 10	No. 10 (1997) 1999 1999 1999 1999 1999 1999 1999	4532 4532	144 24 24 24 24 24 24 24	0.2006 0.0006	6.539 6.669 6.762 6.762 6.562 6.562 6.562 6.562 6.563 6.663 6.563	Selection of the control of the cont		His cone 334 orașe protest Manigario periorea Manigario periorea
1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	N N N N N N N N N N	6537 6537 6537 6537 6537 6537 6537 6537	144 24	0.006 0.006 0.006 0.011 0.016 0.012 0.016 0.007	6.539 6.397 6.392 6.393	Section of the control of the contro	A control of the cont	IN COMM 25 COMMAND AND ADMINISTRATION OF THE
1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	N N N N N N N N N N	653 453 453 453 453 453 453 453 453 453 4	144 245 246 247	0.006 0.006 0.006 0.011 0.006 0.011 0.006 0.007 0.006 0.007 0.006 0.007 0.006 0.007 0.006 0.007 0.006 0.007 0.006 0.007 0.006 0.007 0.006 0.007 0.006	6.539 6.397 6.392 6.393	Section of the control of the contro	A control of the cont	He down 316 organ prices 128 dispersion personne 128 dispersion personne 128 comparation 128 c
1. March 2011	N. S.	6537 6537 6537 6537 6537 6537 6537 6537	144 15	0.016	6.539 6.001 6.002 6.539	Mills	A control of the cont	He down 316 organ prices 128 dispersion personne 128 dispersion personne 128 comparation 128 c
5.05 1.	No. 1	6152 4153 4153 4153 4153 4153 4153 4153 4153	148 152 153 154	0.000 0.001 0.001 0.001 0.001 0.000	6.309 6.000	Mills	B. Commonwealth of the com	His cone 334 orașe protest Manigario periorea Manigario periorea
5.05 1.	N. S.	6152 4153 4153 4154 4154 4155	He He He He He He He He	0.000 0.001 0.001 0.001 0.001 0.000	6.309 6.000	Mills	B. Commonwealth of the com	He down 316 organ prices 128 dispersion personne 128 dispersion personne 128 comparation 128 c
5.05 1.	No. 1	6152 4153 4153 4154 4154 4155	148 152 153 154	0.000 0.001 0.001 0.001 0.001 0.000	6.309 6.000	Mills	B. Commonwealth of the com	Microse Microse aprilione to mitigating performance 11 Compart performance 12 Compart performance 13 Compart performance 14 Compart performance 15 Compart performance
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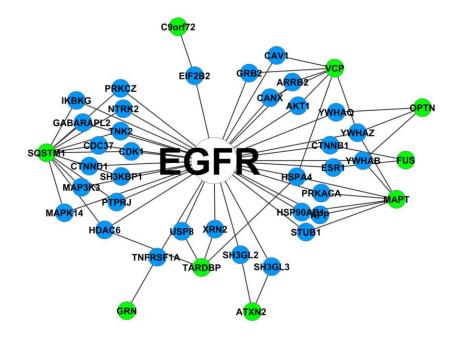
DNA-DAMAGE CONTROL	GENE EXPR	ESSION	GENE EXF	RESSION	WASTE
(BLACK)	(BLAC	K)	(PUF	RPLE)	(PURPLE)
Q9Y2T1	O43707	P51610	Q9Y4W6	P48556	Q9UKV5
O60885	000468	014964	Q12955	P61289	O43681
P24385	P32121	P48551	P05067-APP	P60484	P54252
O75909	Q99700	Q12906	O60306	Q13610	P51572
Q99741	Q9Y2T1	Q92993	Q14865	P78406	Q9NZS9
P49674	Q5H9F3	Q9Y2K7	O00327	P62826	Q96A33
Q01094	O60885	Q92945	Q6PL18	P06400	O43889
Q16254	Q9HCU9	O15525	P54252	Q16576	Q9BUN8
Q09472-EP300	O95503	P61244	Q92934	Q96PK6	Q9GZP9
P18074	P24385	P56270	Q96RK4	Q9NVW2	P31689
Q5XUX0	075909	Q9UIS9	Q9H6U6	P62979	P25685
Q7Z6Z7	Q99741	Q96EZ8	Q96G01	076021	P05198
Q92993	Q9HCK8	Q96RN5	Q6RI45	Q92541	Q96HE7
Q9Y2K7	Q96RK0	075448	Q9Y297	Q96T21	P14625
Q96EZ8	Q99829	Q7Z7M0	Q07021	P28370	Q92598
O00255	Q10570	O00255	Q86VP6	P63162	Q8TAT6
P14174	Q8N684	P14174	Q14444	P18583	Q13438
Q14686	P49674	Q9НВН9	P22681	P35711	P17980
P24928	O60716	Q9HAP2	O95931	Q9UJZ1	P62195
O75807	Q8TDD1	Q99583	P78396	Q13033	Q9BV68
Q99873	P26358	Q7Z7H8	P13987	Q9Y5B9	Q96GF1
P54725	Q01094	Q9BQG0	Q9HD42	Q9BSH4	P60468
Q96PK6	Q16254	Q14686	Q969X6	Q6P1X5	Q9UBV2
Q12824	Q96KS0	Q9Y618	Q9UIV1	Q9UHD2	Q8NHG7
Q08945	Q9Y262	Q15653	P61201	Q15369	O14656
O43463	Q09472-EP300	Q9Y3T9	Q16630	Q12888	O60858
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P63279	Q92800	Q5SRE5	P46108	Q8WWH5	Q9UMX0
O14933	Q14254	Q8IZL8	P19784	Q99816	P54578
Q92900	Q12789	O15534	Q12996	Q9NUQ3	Q9UHP3
Q9P1Z0	O00178	O15055	Q13617	P51668	095292
	O00541	P09012	Q9P013	Q05086	P55072-VCP
	Q99623	Q02086	Q9NQC7	P22695	P17861
	Q9BY77	Q12772	P53355	Q9Y4E8	
	P24928	Q9UQ35	O43293	Q93009	
	O75807	Q08945	000571	Q93008	
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	P46779	P49411	P17181	P05198	
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	Q9Y467	P63279	Q9NV31	Q9BQ52	
	Q5PRF9	P68036	P48200	Q15717-ELAVL	L
	Q9H4L4	Q92900	Q15046	Q96HE7	
	Q15637	075604	Q9Y4X4	P51116	
	Q15459	Q9UPT9	Q13601	P15170	
	Q15393	Q969T9	Q92615	Q8IYD1	
	Q96ST3	000308	Q9Y2U8	P32780	
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	O15105	Q8TF68	P28482	P49773	
	P51532	Q96KM6	P45983	Q9NP66	
	Q12824	Q6ZN55	Q7Z7M0	Q92598	
	(1000 TO 100 TO		Q9NPJ1	Q8N1F7	
			P42568	P52948	
	1		Q9UH92	O15530	
			Q13084	P19387	
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			075592	P54619	
			Q09161	P10644	
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			Q9Y6Q9	014744	
	1		Q99608	F7VJQ1	
			Q96PU5	P25788	
			Q15843	P25789	
			P21359	014818	
			P55769	P49720	
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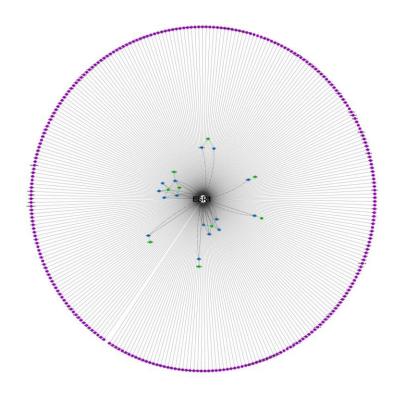
Entrez	A SwissA	NameA	NameA EntrezB SwissB NameB		Taxid.interactor.A	Taxid.interactor.B	Method	Author	PubMed ID	
8945	Q9Y297	BTRC BTRCP FBW1A FBXW1A	468	P18848	ATF4 CREB2 TXREB	taxid:9606(Human)	taxid:9606(Human)	psi-mi:MI:0686(unspecified method)	Pons et al.(2008)	pubmed:1805225
196	P35869	AHR BHLHE76	mouse	P00184	mouse	taxid:9606(Human)	taxid:10090(Mouse)	psi-mi:MI:0686(unspecified method)	Vasiliou et al. (1995)	pubmed:2550446 pubmed:8849333
										pubmed:11382553 pubmed:8215422
										pubmed:1312672 pubmed:7506016 pubmed:2173716
26574	Q9NY61	AATF CHE1 DED HSPC277	TrEMBL	D6RA96	TrEMBL	taxid:9606(Human)	taxid:9606(Human)	psi-mi:"MI:0007"(anti tag coimmunoprecipitation)	Hein et al.	pubmed:unassigned1268 imex:IM-24272

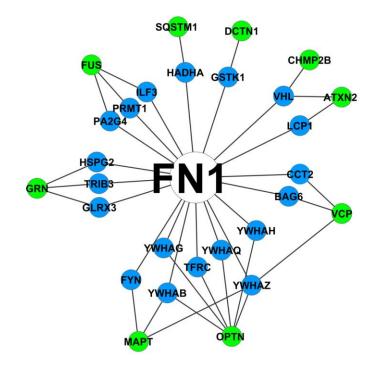




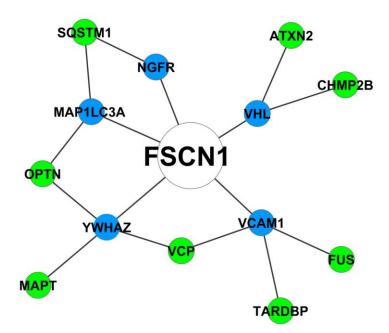


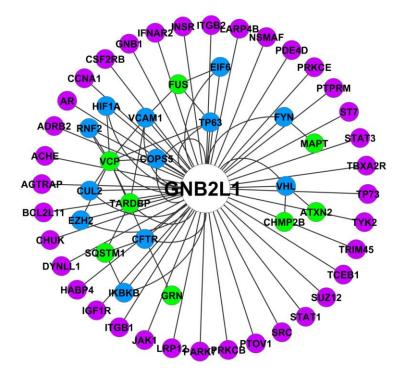




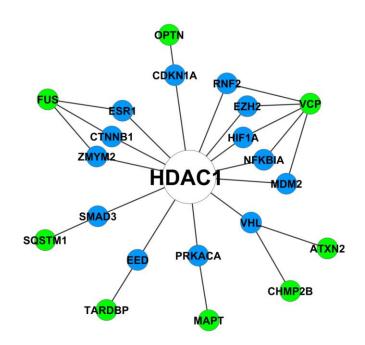


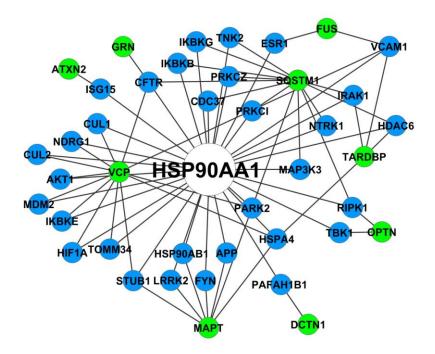
Supporting Figure S8

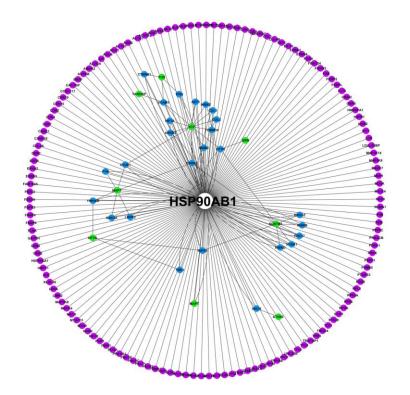


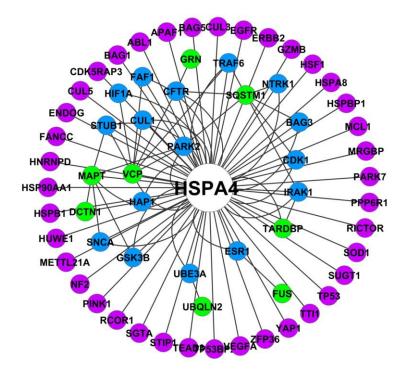


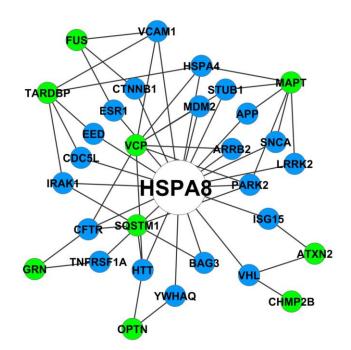
Supporting Figure S10

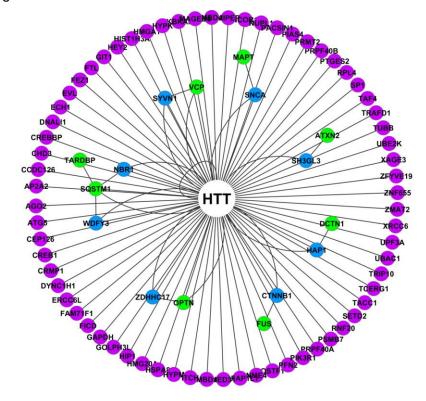




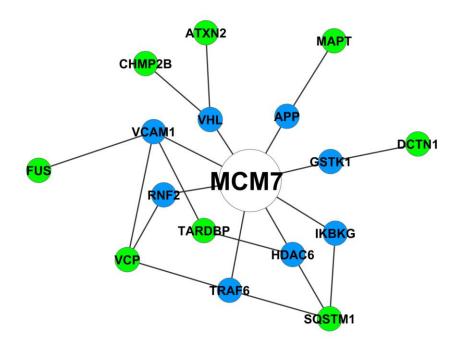


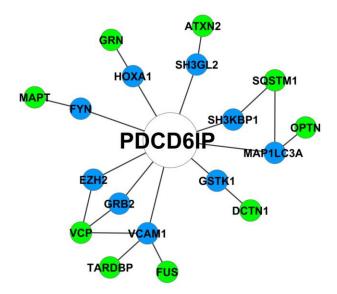


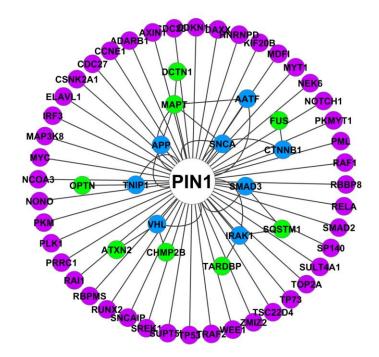


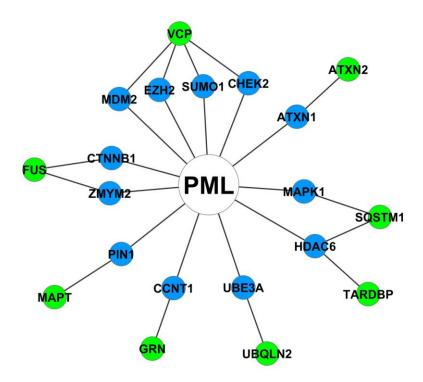


Supporting Figure S16

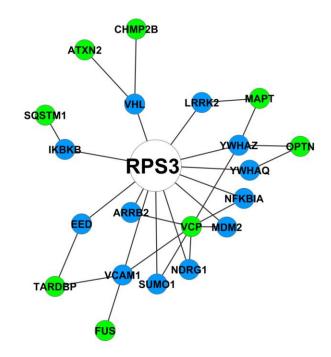


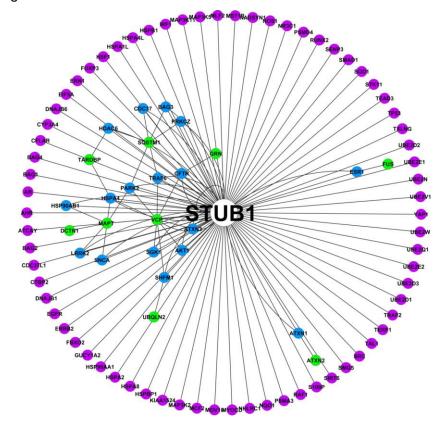


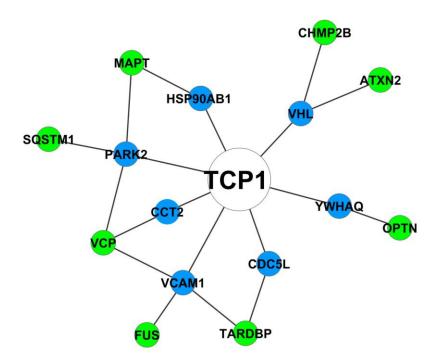


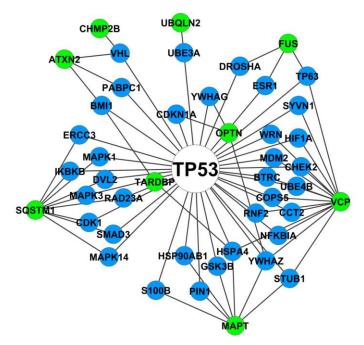


Supporting Figure S20

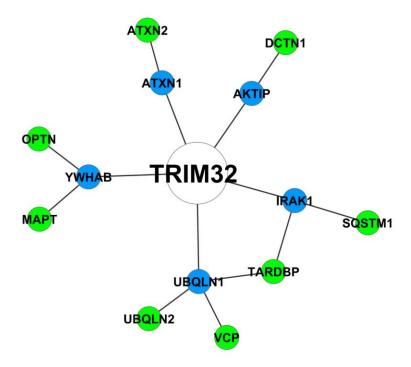


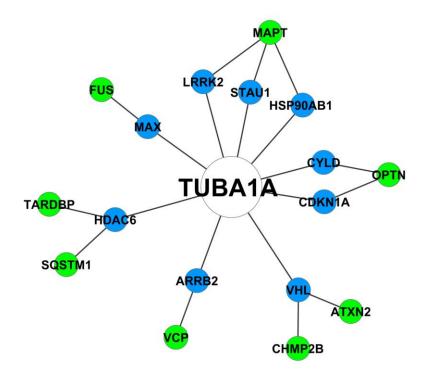


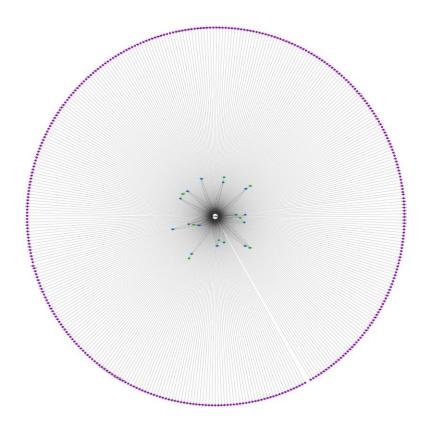


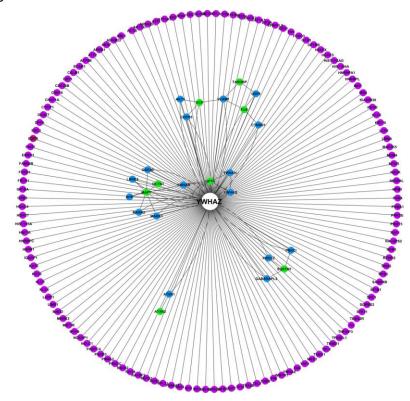


Supporting Figure S24

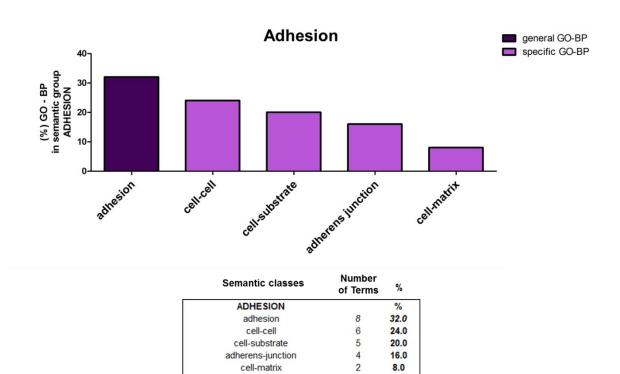








Supporting Figure S28



24.0

20.0

16.0 8.0

100

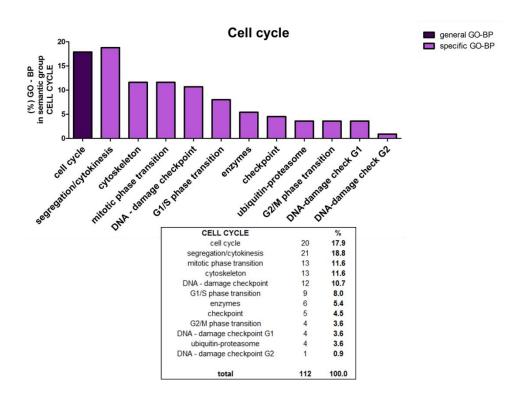
25

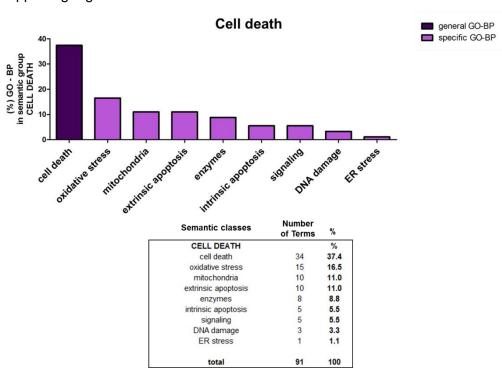
cell-cell

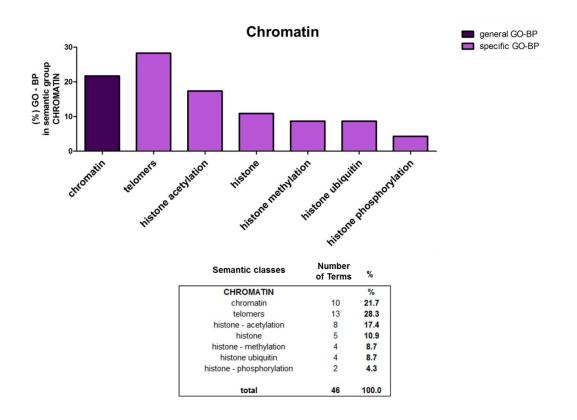
cell-substrate

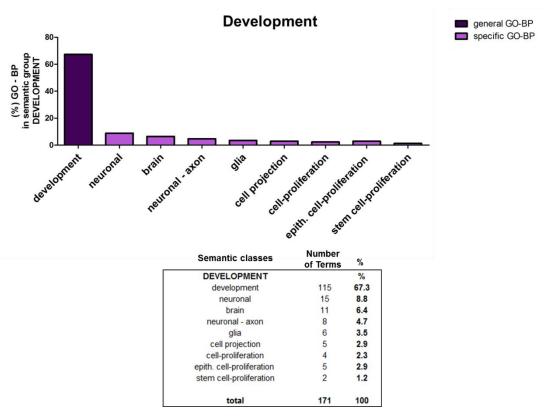
adherens-junction cell-matrix

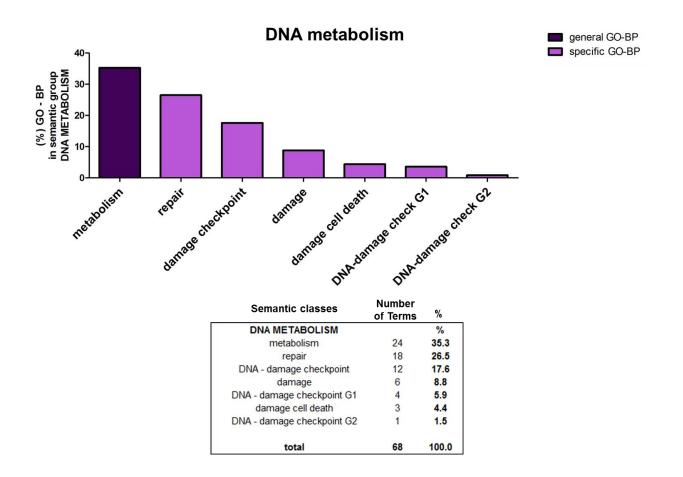
total

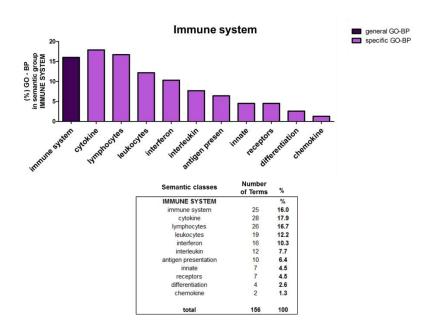


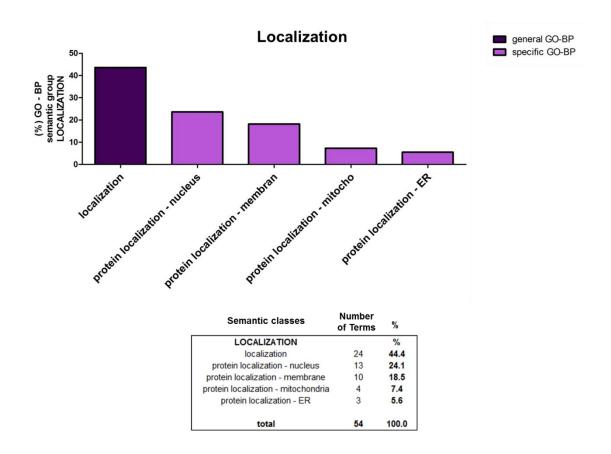


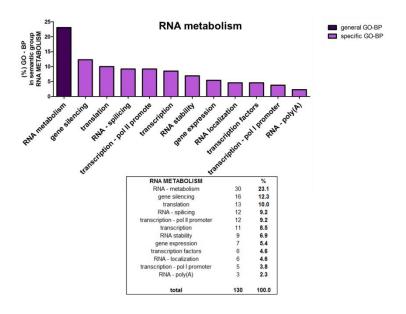


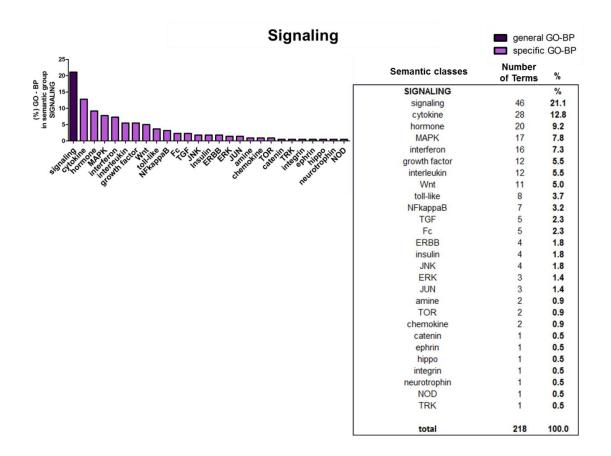


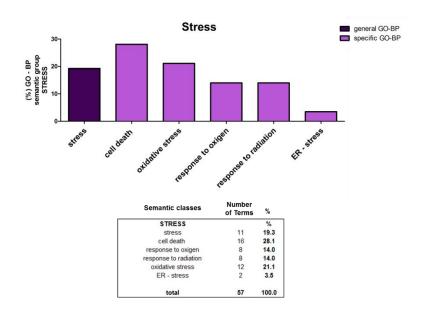


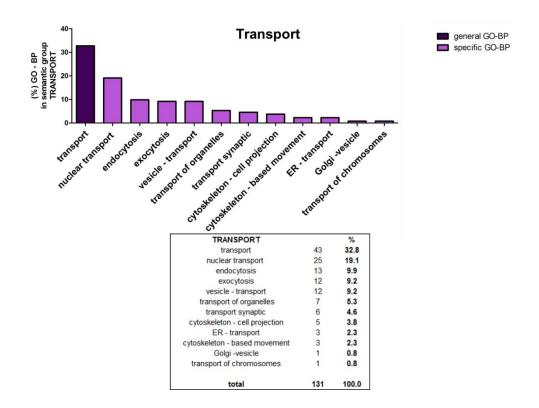


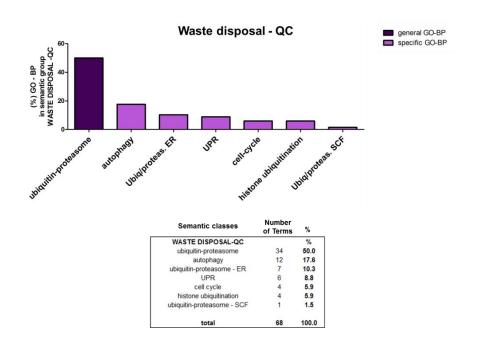


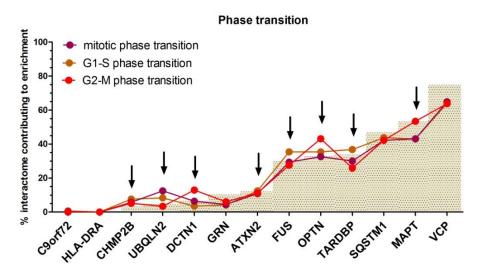


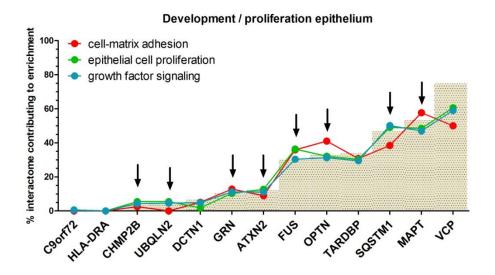


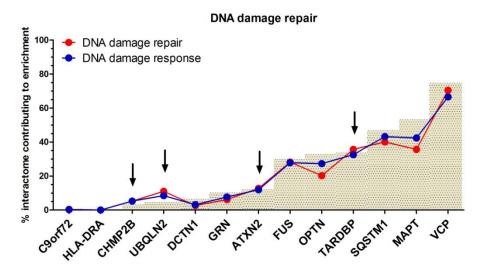


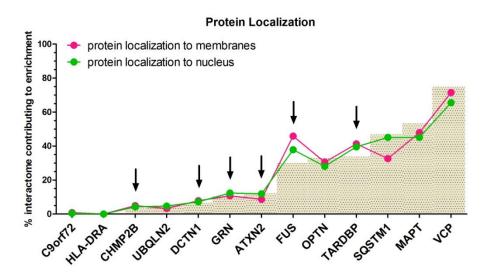












	ATXN2	DCT1N	FUS	GRN	MAPT	OPTN	SQSTM1	TARDBP	UBQLN2	VCP
intrinsic apoptosis after DNA damage	23.8	4.8	31.7	11.1	54.0	39.7	52.4	41.3	9.5	68.3
DNA damage checkpoint	12.0	5.6	30.4	4.0	44.8	35.2	44.8	32.8	5.6	69.6
cell cycle checkpoint	11.2	4.8	29.6	4.0	42.4	32.8	42.4	32.8	5.6	71.2
DNA damage checkpoint G1	20.0	2.2	35.6	6.7	60.0	55.6	57.8	33.3	8.9	68.9
DNA damage response	11.9	3.2	27.9	7.7	42.4	27.3	43.2	32.6	8.5	66.6
apoptotic signaling	11.6	6.3	29.5	10.3	51.7	36.7	56.4	35.4	5.0	65.5
cell death intrinsic apoptosis	16.0	6.1	30.1	14.1	51.5	33.7	52.8	37.4	7.4	71.8
mitotic phase transition	10.9	6.4	29.4	4.5	43.1	32.6	42.2	30.0	12.5	64.9
G2-M phase transition	11.2	12.9	27.6	6.0	53.4	43.1	42.2	25.9	3.4	63.8
G1-S phase transition	12.5	3.5	35.4	4.2	43.1	35.4	43.8	36.8	8.3	63.9
DNA damage repair	12.8	2.6	28.2	6.2	35.7	20.3	40.1	35.7	11.0	70.5
epithelial cell proliferation	12.7	1.8	36.4	10.3	48.5	32.1	49.1	30.3	5.5	60.6
cell-matrix adhesion	9.0	5.1	35.9	12.8	57.7	41.0	38.5	30.8	0.0	50.0
growth factor signaling	11.2	4.9	30.4	11.2	47.0	31.2	50.1	29.5	4.6	59.0
ER transport	4.0	8.0	8.0	16.0	28.0	8.0	36.0	44.0	16.0	96.0
ER stress	8.8	6.8	22.3	13.5	41.2	20.9	46.6	37.8	16.9	81.8
ER ubiquitin-proteasome	6.2	5.3	17.7	13.3	36.3	18.6	43.4	38.1	18.6	83.2
UPR	11.2	9.2	28.6	25.5	50.0	22.4	46.9	41.8	11.2	78.6
response to oxidative stress	18.6	7.2	34.7	12.6	51.5	29.9	54.5	38.3	7.8	65.9
response to ionizing radiation	9.7	3.1	30.1	8.7	39.8	27.6	45.9	35.2	5.1	68.9
gene expression	10.1	3.4	31.6	6.6	37.5	22.2	36.6	30.9	3.6	57.9
translation	10.9	3.0	43.9	2.8	44.4	15.5	27.9	41.1	1.5	66.5
transcription	10.8	3.1	29.6	8.4	35.6	24.3	40.3	27.7	3.6	58.0
transcription-RNA pol II	12.5	2.8	32.1	8.7	33.8	21.4	41.4	27.1	4.3	58.0
protein localization to membrane	8.7	7.9	45.9	10.7	47.9	30.6	32.6	41.3	3.3	71.5
protein localization to nucleus	11.9	7.2	37.9	12.3	45.1	28.1	45.1	39.6	4.7	65.5